



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(21) International Application Number:</b> PCT/IB98/01939 <b>(22) International Filing Date:</b> 27 November 1998 (27.11.98)  <b>(30) Priority Data:</b> 97/15041           28 November 1997 (28.11.97)   FR 97/16034           17 December 1997 (17.12.97)   FR 60/107,077          4 November 1998 (04.11.98)   US  <b>(71) Applicant (for all designated States except US):</b> GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR).  <b>(72) Inventor; and</b> <b>(75) Inventor/Applicant (for US only):</b> GRIFFAIS, Rémy [FR/FR]; 51, boulevard Romain Roland, F-92120 Montrouge (FR).  <b>(74) Agents:</b> MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).		<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
<b>(54) Title:</b> <i>CHLAMYDIA TRACHOMATIS</i> GENOMIC SEQUENCE AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF INFECTION  <b>(57) Abstract</b> <p>The subject of the invention is the genomic sequence and the nucleotide sequences encoding polypeptides of <i>Chlamydia trachomatis</i>, such as cellular envelope polypeptides, which are secreted or specific, or which are involved in metabolism, in the replication process or in virulence, polypeptides encoded by such sequences, as well as vectors including the said sequences and cells or animals transformed with these vectors. The invention also relates to transcriptional gene products of the <i>Chlamydia trachomatis</i> genome, such as, for example, antisense and ribozyme molecules, which can be used to control growth of the microorganism. The invention also relates to methods of detecting these nucleic acids or polypeptides and kits for diagnosing <i>Chlamydia trachomatis</i> infection. The invention also relates to a method of selecting compounds capable of modulating bacterial infection and a method for the biosynthesis or biodegradation of molecules of interest using the said nucleotide sequences or the said polypeptides. The invention finally comprises, pharmaceutical, in particular vaccine, compositions for the prevention and/or treatment of bacterial, in particular <i>Chlamydia trachomatis</i>, infections.</p>		

The DNA sequence encoding the antigenic polypeptide and regulatory element may be inserted into a stable cell line or cloned microorganism, using techniques, such as targeted homologous recombination, which are well known to those of skill in the art, and described *e.g.*, in Chappel, U.S. Patent No. 4,215,051; Skoultchi, WO 91/06667 each of which is incorporated herein by  
5 reference in its entirety.

Such cell lines and microorganisms may be formulated for vaccine purposes. In yet another embodiment, the DNA sequence encoding the antigenic polypeptide and regulatory element may be delivered to a mammalian host and introduced into the host genome via homologous recombination (*See*, Chappel, U.S. Patent No. 4,215,051; Skoultchi, WO 91/06667 each of which is  
10 incorporated herein by reference in its entirety.

Preferably, the immunogenic and/or vaccine compositions according to the invention intended for the prevention and/or the treatment of an infection by *Chlamydia pneumoniae* or by an associated microorganism will be chosen from the immunogenic and/or vaccine compositions comprising a polypeptide or one of its representative fragments corresponding to a protein, or one of  
15 its representative fragments, of the cellular envelope of *Chlamydia pneumoniae*. The vaccine compositions comprising nucleotide sequences will also preferably comprise nucleotide sequences encoding a polypeptide or one of its representative fragments corresponding to a protein, or one of its representative fragments, of the cellular envelope of *Chlamydia pneumoniae*.

Among these preferred immunogenic and/or vaccine compositions, the most preferred are  
20 those comprising a polypeptide or one of its representative fragments, or a nucleotide sequence or one of its representative fragments whose sequences are chosen from the nucleotide or amino acid sequences identified in this functional group and listed above.

The polypeptides of the invention or their representative fragments entering into the immunogenic compositions according to the invention may be selected by techniques known to  
25 persons skilled in the art, such as for example on the capacity of the said polypeptides to stimulate T cells, which results, for example, in their proliferation or the secretion of interleukins, and which leads to the production of antibodies directed against the said polypeptides.

In mice, in which a weight dose of the vaccine composition comparable to the dose used in humans is administered, the antibody reaction is tested by collecting serum followed by a study of  
30 the formation of a complex between the antibodies present in the serum and the antigen of the vaccine composition, according to the customary techniques.

According to the invention, the said vaccine compositions will be preferably in combination with a pharmaceutically acceptable vehicle and, where appropriate, with one or more appropriate immunity adjuvants.

35 Various types of vaccines are currently available for protecting humans against infectious diseases: attenuated live microorganisms (*M. bovis* - BCG for tuberculosis), inactivated microorganisms (influenza virus), acellular extracts (*Bordetella pertussis* for whooping cough),

recombinant proteins (hepatitis B virus surface antigen), polysaccharides (pneumococci). Experiments are underway on vaccines prepared from synthetic peptides or from genetically modified microorganisms expressing heterologous antigens. Even more recently, recombinant plasmid DNAs carrying genes encoding protective antigens were proposed as an alternative vaccine strategy. This type of vaccination is carried out with a particular plasmid derived from an *E. coli* plasmid which does not replicate *in vivo* and which encodes only the vaccinal protein. Animals were immunized by simply injecting the naked plasmid DNA into the muscle. This technique leads to the expression of the vaccine protein *in situ* and to a cell-type (CTL) and a humoral type (antibody) immune response. This double induction of the immune response is one of the main advantages of the technique of vaccination with naked DNA.

The vaccine compositions of the present invention can be evaluated in *in vitro* and *in vivo* animal models prior to host, e.g., human, administration. For example, *in vitro* neutralization assays such as those described by Peterson et al. (1988) can be utilized. The assay described by Peterson et al. (1988) is suitable for testing vaccine compositions directed toward either *Chlamydia pneumoniae* or *Chlamydia trachomatis*.

Briefly, hyper-immune antisera is diluted in PBS containing 5% guinea pig serum, as a complement source. *Chlamydiae* ( $10^4$  IFU; infectious units) are added to the antisera dilutions. The antigen-antibody mixtures are incubated at 37EC for 45 minutes and inoculated into duplicate confluent Hep-2 or HeLa cell monolayers contained in glass vials (e.g., 15 by 45 mm), which have been washed twice with PBS prior to inoculation. The monolayer cells are infected by centrifugation at 1000X g for 1 hour followed by stationary incubation at 37E for 1 hour. Infected monolayers are incubated for 48 or 72 hours, fixed and stained with a *Chlamydiae* specific antibody, such as anti-MOMP for *C. trachomatis*, etc. IFUs are counted in ten fields at a magnification of 200X. Neutralization titer is assigned based on the dilution that gives 50% inhibition as compared to control monolayers/IFU.

The efficacy of vaccine compositions can be determined *in vivo* by challenging animal models of *Chlamydia pneumoniae* infection, e.g., mice or rabbits, with the vaccine compositions. For example, *in vivo* vaccine composition challenge studies can be performed in the murine model of *Chlamydia pneumoniae* infection described by Moazed et al. (1997). Briefly, male homozygous apoE deficient and/or C57 BL/6J mice are immunized with vaccine compositions. Post-vaccination, the mice are mildly sedated by subcutaneous injection of a mixture of ketamine and xylazine, and inoculated intranasally with a total volume of 0.03-0.05 ml of organisms suspended in SPG medium or with SPG alone. The inoculations of *Chlamydia pneumoniae* are approximately  $3 \times 10^7$  IFU/mouse. The mice are inoculated with *Chlamydia pneumoniae* at 8, 10, and 12 weeks of age. Tissues are then collected from the lung, spleen, heart, etc. at 1-20 weeks after the first inoculation. The presence of organisms is scored using PCR, histology and immunocytochemistry, or by quantitative culture/IFU after tissue homogenization.

Alternatively, *in vivo* vaccine composition challenge studies can be performed in the rabbit model of *Chlamydia pneumoniae* described by Laitinen et al. (1997). Briefly, New Zealand white rabbits (5 months old) are immunized with the vaccine compositions. Post-vaccination, the rabbits are sedated with Hypnorm, 0.3 ml/Kg of body weight, intramuscularly, and inoculated  
5 intranasally with a total of 0.5 ml of *Chlamydia pneumoniae* suspended in SPG medium or with SPG alone. The inoculations of *Chlamydia pneumoniae* are approximately  $3 \times 10^7$  IFU/rabbit. The rabbits are reinfected in the same manner and with the same dose 3 weeks after the primary inoculation. Tissues are then collected 2 weeks after the primary infection and 1, 2, and 4 weeks after the reinfection. The presence of *Chlamydia pneumoniae* is scored using PCR, histology and  
10 immunocytochemistry, or by quantitative culture/IFU after tissue homogenization.

The vaccine compositions comprising nucleotide sequences or vectors into which the said sequences are inserted are in particular described in International Application No. WO 90/11092 and also in International Application No. WO 95/11307.

The nucleotide sequence constituting the vaccine composition according to the invention  
15 may be injected into the host after having been coupled to compounds which promote the penetration of this polynucleotide inside the cell or its transport up to the cell nucleus. The resulting conjugates may be encapsulated into polymeric microparticles, as described in International Application No. WO 94/27238 (Medisorb Technologies International).

According to another embodiment of the vaccine composition according to the invention,  
20 the nucleotide sequence, preferably a DNA, is complexed with the DEAE-dextran (Pagano et al., 1967) or with nuclear proteins (Kaneda et al., 1989), with lipids (Felgner et al., 1987) or encapsulated into liposomes (Fraley et al., 1980) or alternatively introduced in the form of a gel facilitating its transfection into the cells (Midoux et al., 1993, Pastore et al., 1994). The polynucleotide or the vector according to the invention may also be in suspension in a buffer solution or may be combined with  
25 liposomes.

Advantageously, such a vaccine will be prepared in accordance with the technique described by Tacson et al. or Huygen et al. in 1996 or alternatively in accordance with the technique described by Davis et al. in International Application No. WO 95/11307.

Such a vaccine may also be prepared in the form of a composition containing a vector  
30 according to the invention, placed under the control of regulatory elements allowing its expression in humans or animals. It is possible, for example, to use, as vector for the *in vivo* expression of the polypeptide antigen of interest, the plasmid pcDNA3 or the plasmid pcDNA1/neo, both marketed by Invitrogen ® & D Systems, Abingdon, United Kingdom). It is also possible to use the plasmid V1Jns.tPA, described by Shiver et al. in 1995. Such a vaccine will advantageously comprise, in  
35 addition to the recombinant vector, a saline solution, for example a sodium chloride solution.

The immunogenic compositions of the invention can also be utilized as part of methods for immunization, wherein such methods comprise administering to a host, *e.g.*, a human host, an

immunizing amount of the immunogenic compositions of the invention. In a preferred embodiment, the method of immunizing is a method of immunizing against *Chlamydia pneumoniae*.

A pharmaceutically acceptable vehicle is understood to designate a compound or a combination of compounds entering into a pharmaceutical or vaccine composition which does not  
5 cause side effects and which makes it possible, for example, to facilitate the administration of the active compound, to increase its life and/or its efficacy in the body, to increase its solubility in solution or alternatively to enhance its preservation. These pharmaceutically acceptable vehicles are well known and will be adapted by persons skilled in the art according to the nature and the mode of administration of the active compound chosen.

10 As regards the vaccine formulations, these may comprise appropriate immunity adjuvants which are known to persons skilled in the art, such as, for example, aluminum hydroxide, a representative of the family of muramyl peptides such as one of the peptide derivatives of N-acetyl-muramyl, a bacterial lysate, or alternatively incomplete Freund's adjuvant, Stimulon™ QS-21 (Aquila Biopharmaceuticals, Inc., Framingham, MA), MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI  
15 ImmunoChem Research, Inc., Hamilton, MT), aluminum phosphate, IL-12 (Genetics Institute, Cambridge, MA).

Preferably, these compounds will be administered by the systemic route, in particular by the intravenous route, by the intranasal, intramuscular, intradermal or subcutaneous route, or by the oral route. More preferably, the vaccine composition comprising polypeptides according to the  
20 invention will be administered several times, spread out over time, by the intradermal or subcutaneous route.

Their optimum modes of administration, dosages and galenic forms may be determined according to criteria which are generally taken into account in establishing a treatment adapted to a patient, such as for example the patient's age or body weight, the seriousness of his general condition,  
25 tolerance of the treatment and the side effects observed.

The invention comprises the use of a composition according to the invention for the treatment or the prevention of cardiovascular diseases, preferably linked to the presence of atheroma, which are induced or worsened by *Chlamydia pneumoniae*.

Finally, the invention comprises the use of a composition according to the invention for  
30 the treatment or the prevention of respiratory diseases which are induced or worsened by the presence of *Chlamydia pneumoniae*, preferably asthma.

Other characteristics and advantages of the invention appear in the following examples and figures:

35 Legend to the figures :

Figure 1 : Line for the production of *Chlamydia pneumoniae* sequences

TABLE 1							I%
ORF	Begin	End	Homology	ID	Species	Score	
ORF2	42	794	triosephosphate isomerase	L27492	<i>Thermotoga maritima</i>	567	54
ORF3	1258	1614	putative				
ORF4	1807	2418	polypeptide deformylase	D90906	<i>Synechocystis sp.</i>	316	40
ORF5	3393	2491	hypothetical protein	Z75208	<i>Bacillus subtilis</i>	338	42
ORF6	3639	4067	unknown	U87792	<i>Bacillus subtilis</i>	117	38
ORF7	5649	4270	putative				
ORF8	7463	6012	putative				
ORF9	8051	8962	putative				
ORF10	9129	9959	putative				
ORF11	10687	10361	putative				
ORF12	10927	11232	putative				
ORF13	11246	12727	amidase	U49269	<i>Moraxella catarrhalis</i>	1108	42
ORF14	12691	14190	PET112	D90913	<i>Synechocystis sp.</i>	1044	46
ORF15	14484	17249	POMP91A	U65942	<i>Chlamydia psittaci</i>	1074	43
ORF16	16039	15770	putative				
ORF17	17845	20853	putative				
ORF18	21137	22042	putative				
ORF19	22046	23476	putative				
ORF20	23681	26110	putative				
ORF21	26109	25861	putative				
ORF22	26241	26978	putative				
ORF23	26960	27754	putative				
ORF24	27747	28577	putative				
ORF25	28887	29492	POMP91A	U65942	<i>Chlamydia psittaci</i>	180	39
ORF26	29432	30028	POMP91A	U65942	<i>Chlamydia psittaci</i>	361	51
ORF27	30024	31472	POMP91A	U65942	<i>Chlamydia psittaci</i>	879	54
ORF28	31758	32288	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	144	43
ORF29	32201	33991	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1126	48
ORF30	33852	34541	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	589	62
ORF31	34783	36063	POMP91B precursor	U65943	<i>Chlamydia psittaci</i>	469	46
ORF32	36009	37529	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1338	51
ORF33	37881	39362	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	671	40

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF34	39418	39161	putative				
ORF35	39366	40715	POMP90A precursor	U65942	<i>Chlamydia psittaci</i>	904	47
ORF36	43076	41094	putative				
ORF37	43800	43066	putative				
ORF38	44828	43785	putative				
ORF39	45340	44753	homologous to unidentified E. coli protein	M96343	<i>Bacillus subtilis</i>	136	44
ORF40	45752	45372	o530; This 530 aa orf is 33 pct identical (14 gaps) to 525 residues of an approx. 640 aa protein YHES HAEIN SW: P44808	AE000184	<i>Escherichia coli</i>	269	43
ORF41	46996	45701	ABC transporter, ATP-binding protein (yheS)	AE000596	<i>Helicobacter pylori</i>	878	39
ORF42	47961	47569	putative				
ORF43	48960	48040	hypothetical protein	D64001	<i>Synechocystis</i> sp.	404	37
ORF44	51452	50133	Lon protease-like protein	X74215	<i>Homo sapiens</i>	1232	54
ORF45	52606	51335	unknown	Z54285	<i>Schizosaccharomyces pombe</i>	781	47
ORF46	53684	53319	putative				
ORF47	54195	53746	putative				
ORF48	55278	56453	heat-shock protein	U15010	<i>Legionella pneumophila</i>	975	45
ORF49	56493	57266	branched chain alpha-keto acid dehydrogenase E1-alpha	M97391	<i>Bacillus subtilis</i>	329	36
ORF50	57297	58526	branched chain alpha-keto acid dehydrogenase E1-beta	M97391	<i>Bacillus subtilis</i>	707	50
ORF51	59851	58565	putative				
ORF52	61495	59924	ComE	D90903	<i>Synechocystis</i> sp.	134	55
ORF53	61324	62151	putative				
ORF54	62132	62470	Hpr protein	X12832	<i>Bacillus subtilis</i>	136	36
ORF55	62474	63733	enzyme I (ptsI)	U32844	<i>Haemophilus influenzae</i>	381	35
ORF56	63881	64186	f831; This 831 aa orf is 46 pct identical (11 gaps) to 709 residues of an approx. 712 aa protein PT1A ECOLI SW: P32670	AE000326	<i>Escherichia coli</i>	123	34
ORF57	64611	64318	ORF107	X17014	<i>Bacillus subtilis</i>	128	33
ORF58	65485	64673	putative				
ORF59	65999	65301	dnaZX-like ORF put. DNA polymerase III	X06803	<i>Bacillus subtilis</i>	596	52



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF60	66244	67281	putative				
ORF61	67265	67699	putative				
ORF62	67703	68539	putative				
ORF63	68805	70736	putative				
ORF64	69172	68831	putative				
ORF65	70642	71142	putative				
ORF66	71325	72029	putative				
ORF67	72060	73637	putative				
ORF68	74061	76175	Yqff	D84432	<i>Bacillus subtilis</i>	542	44
ORF69	78351	77680	porphobilinogen deaminase	D28503	<i>Clostridium josui</i>	262	42
ORF70	79356	78355	sms protein	D90914	<i>Synechocystis</i> sp.	736	52
ORF71	79983	79693	ribonuclease III (mc)	AE000579	<i>Helicobacter pylori</i>	98	33
ORF72	80441	79938	ORF3	D64116	<i>Bacillus subtilis</i>	268	44
ORF73	80475	80969	putative				
ORF74	81296	83080	hypothetical protein	Y14079	<i>Bacillus subtilis</i>	893	38
ORF75	83291	83932	manganese superoxide dismutase	X77021	<i>Caenorhabditis elegans</i>	622	58
ORF76	84005	84769	acetyl-CoA carboxylase beta subunit (accD)	AE000604	<i>Helicobacter pylori</i>	602	50
ORF77	84975	85244	deoxyuridinetriphosphatase (dut)	U32776	<i>Haemophilus influenzae</i>	110	41
ORF78	85123	85425	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)	AE000596	<i>Helicobacter pylori</i>	265	68
ORF79	85397	85903	ORF2	L26916	<i>Pseudomonas aeruginosa</i>	173	34
ORF80	85909	86583	enzyme IIANtr	U18997	<i>Escherichia coli</i>	170	42
ORF81	86626	88065	putative				
ORF82	89257	91026	putative				
ORF83	91291	93030	putative				
ORF84	93295	94086	putative				
ORF85	95285	94707	putative				
ORF86	95667	96557	putative				
ORF87	96317	97456	putative				
ORF88	98435	97968	putative				
ORF89	99460	98426	putative				
ORF90	100144	101325	elongation factor Tu	L22216	<i>Chlamydia trachomatis</i>	1917	95



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF91	101457	101720	putative				
ORF92	101704	102273	transcription factor	L10348	<i>Thermus aquaticus thermophilus</i>	376	49
ORF93	102356	102805	ribosomal protein L11	D13303	<i>Bacillus subtilis</i>	458	63
ORF94	102835	103530	ribosomal protein L1	Z11839	<i>Thermotoga maritima</i>	642	51
ORF95	103549	104058	ribosomal protein L10	M89911	<i>Streptomyces antibioticus</i>	82	31
ORF96	104096	104491	rp12 (AA 1-128)	X53178	<i>Synechocystis PCC6803</i>	325	47
ORF97	104601	108386	DNA-directed RNA polymerase beta chain	X64172	<i>Staphylococcus aureus</i>	2740	52
ORF98	108401	112054	rpoC	V00339	<i>Escherichia coli</i>	2947	54
ORF99	112033	112590	acetylornithine deacetylase (EC 5.1.1.16)	M22622	<i>Leptospira biflexa</i>	514	62
ORF100	112672	113682	transaldolase	L19437	<i>Homo sapiens</i>	755	49
ORF101	113726	114121	putative				
ORF102	114711	114136	putative				
ORF103	115267	115755	putative				
ORF104	115911	116543	putative				
ORF105	116736	118055	ATPase alpha-subunit	X63855	<i>Thermus aquaticus thermophilus</i>	934	50
ORF106	117968	118522	adenosine triphosphatase A subunit	D50528	<i>Acetabularia acetabulum</i>	147	32
ORF107	118530	119843	V-ATPase B subunit	U96487	<i>Desulfurococcus sp. SY</i>	751	48
ORF108	119816	120457	putative				
ORF109	120451	122430	v-type Na-ATPase	X76913	<i>Enterococcus hirae</i>	264	35
ORF110	122504	122950	ATP synthase, subunit K	U67478	<i>Methanococcus jannaschii</i>	184	31
ORF111	123528	126347	valyl-tRNA synthetase	X05891	<i>Escherichia coli</i>	1679	49
ORF112	126332	129166	protein kinase-like protein	U19250	<i>Streptomyces coelicolor</i>	427	37
ORF113	134690	129213	UvrA	D49911	<i>Thermus thermophilus</i>	3107	41
ORF114	134925	136382	pyruvate kinase	U83196	<i>Chlamydia trachomatis</i>	1748	71
ORF115	137870	136482	HtrB protein	X61000	<i>Escherichia coli</i>	147	38
ORF116	137899	138240	putative				
ORF117	138239	137928	putative				
ORF118	139558	138257	putative				
ORF119	140352	139516	YbbP	AB002150	<i>Bacillus subtilis</i>	231	46
ORF120	140498	141841	cyanide insensitive terminal oxidase	Y10528	<i>Pseudomonas aeruginosa</i>	538	50
ORF121	141855	142658	cyanide insensitive terminal oxidase	Y10528	<i>Pseudomonas aeruginosa</i>	310	40
ORF122	144258	143050	putative				
ORF123	145258	144494	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF124	145454	146749	product similar to E. coli PhoH protein	Z97025	<i>Bacillus subtilis</i>	836	47
ORF125	147318	146767	putative				
ORF126	148261	147677	putative				
ORF127	149029	152157	isoleucyl-tRNA synthetase	U04953	<i>Homo sapiens</i>	2361	52
ORF128	154108	152201	leader peptidase I	D90904	<i>Synechocystis sp.</i>	225	47
ORF129	155135	154308	putative				
ORF130	155141	155467	YtiA	AF008220	<i>Bacillus subtilis</i>	201	43
ORF131	155703	156779	orf 361; translated orf similarity to SW: RF1_SALTY peptide chain release factor 1 of <i>Salmonella typhimurium</i>	X78969	<i>Coxiella burnetii</i>	863	59
ORF132	156748	157635	product similar to E. coli PRFA2 protein	Z49782	<i>Bacillus subtilis</i>	144	37
ORF133	157653	158996	Ffh	U82109	<i>Thermus aquaticus</i>	797	45
ORF134	159363	159986	tRNA (guanine-N1)-methyltransferase (trmD)	U32705	<i>Haemophilus influenzae</i>	545	49
ORF135	159880	160446	putative				
ORF136	160477	160839	ribosomal protein L19	X72627	<i>Synechocystis sp.</i>	319	50
ORF137	160898	161539	putative protein highly homologous to E. coli RNase HIII	D32253	<i>Magnetospirillum sp.</i>	427	49
ORF138	161527	162153	5'guanylate kinase (gmk)	U32848	<i>Haemophilus influenzae</i>	385	43
ORF139	162144	162443	putative				
ORF140	162437	164098	methionyl-tRNA synthetase	AB004537	<i>Schizosaccharomyces pombe</i>	861	54
ORF141	165451	164228	exodeoxyribonuclease V (recD)	U32811	<i>Haemophilus influenzae</i>	432	32
ORF142	166349	165411	putative				
ORF143	166949	168442	putative				
ORF144	169416	171029	putative				
ORF145	170857	171459	putative				
ORF146	172652	173428	putative biotin-protein ligase	Z97992	<i>Schizosaccharomyces pombe</i>	292	44
ORF147	174626	173439	putative				
ORF148	174816	175613	putative				
ORF149	175598	175954	putative				
ORF150	175958	176935	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF151	177708	176938	orf 3' of chaperonin homolog hypB [Chlamydia psittaci, pigeon strain P-1041, Peptide Partial, 98 aa]	S40172	<i>Chlamydia psittaci</i>	376	74
ORF152	177128	177376	putative				
ORF153	179472	177841	putative	M69217	<i>Chlamydia pneumoniae</i>	2678	100
ORF154	179822	179517	putative	M69217	<i>Chlamydia pneumoniae</i>	498	99
ORF155	181793	179943	Pz-peptidase	D88209	<i>Bacillus licheniformis</i>	1088	38
ORF156	182628	181876	o247; This 247 aa orf is 51 pct identical (0 gaps) to 117 residues of an approx. 160 aa protein YPH7 CHRVI SW: P45371	AE000174	<i>Escherichia coli</i>	401	42
ORF157	184420	183074	glutamate-1-semialdehyde 2,1- aminomutase	X53696	<i>Escherichia coli</i>	823	41
ORF158	184988	184467	ORF o211	U28377	<i>Escherichia coli</i>	87	54
ORF159	185483	185112	hypothetical protein	D90906	<i>Synechocystis sp.</i>	91	33
ORF160	185902	185483	ribose 5-phosphate isomerase	U28377	<i>Escherichia coli</i>	111	41
ORF161	186174	185839	ribose 5-phosphate isomerase A (SP:P27252)	U32729	<i>Haemophilus influenzae</i>	190	46
ORF162	187720	186587	hypothetical	D83026	<i>Bacillus subtilis</i>	536	42
ORF163	188318	190933	ATP-dependent protease binding subunit	M29364	<i>Escherichia coli</i>	2010	53
ORF164	191090	191635	putative				
ORF165	191547	192743	putative				
ORF166	192969	193469	putative				
ORF167	194044	193610	putative				
ORF168	194196	195809	unknown	Z84395	<i>Mycobacterium tuberculosis</i>	242	52
ORF169	196088	198073	DNA ligase (EC 6.5.1.2)	M24278	<i>Escherichia coli</i>	1317	46
ORF170	198132	199454	putative				
ORF171	199351	202818	putative				
ORF172	204552	202999	PcpB	U60175	<i>Sphingomonas chlorophenolica</i>	80	41
ORF173	205648	204692	putative				
ORF174	205807	207327	leucine tRNA synthetase	AF008220	<i>Bacillus subtilis</i>	1595	57
ORF175	207182	207775	leucyl-tRNA synthetase	X06331	<i>Escherichia coli</i>	363	51
ORF176	207779	208267	transfer RNA-Leu synthetase	M88581	<i>Bacillus subtilis</i>	285	43
ORF177	208267	209577	KDO transferase	Z31593	<i>Chlamydia pneumoniae</i>	2262	100

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF178	211807	211271	KDO-transferase	X80061	<i>Chlamydia psittaci</i>	105	38
ORF179	212188	211844	putative				
ORF180	214079	212448	pyrophosphate-dependent phosphofructokinase beta subunit	Z32850	<i>Ricinus communis</i>	1003	45
ORF181	214907	214083	CinI	U44893	<i>Butyrivibrio fibrisolvens</i>	111	41
ORF182	216154	215429	putative				
ORF183	216115	216678	putative				
ORF184	216728	217282	putative				
ORF185	217267	217866	putative				
ORF186	218593	218261	putative				
ORF187	219821	218994	putative				
ORF188	221382	220309	putative				
ORF189	222719	221433	GMP synthetase	M10101	<i>Escherichia coli</i>	1151	48
ORF190	223521	222724	IMP dehydrogenase	X66859	<i>Acinetobacter calcoaceticus</i>	778	58
ORF191	224499	225008	putative				
ORF192	225140	225559	putative				
ORF193	225555	226802	putative				
ORF194	227800	226892	putative				
ORF195	228335	228072	putative				
ORF196	229251	228643	putative				
ORF197	230983	229622	YqhX	D84432	<i>Bacillus subtilis</i>	1386	56
ORF198	231483	230983	acetyl-CoA carboxylase biotin carboxyl carrier protein	U38804	<i>Porphyra purpurea</i>	199	52
ORF199	232063	231509	elongation factor P	D64001	<i>Synechocystis sp.</i>	282	32
ORF200	232739	232053	pentose-5-phosphate-3-epimerase	D90911	<i>Synechocystis sp.</i>	463	43
ORF201	233166	234356	putative				
ORF202	233518	233165	putative				
ORF203	234536	235186	ORF2	L35036	<i>Chlamydia psittaci</i>	570	60
ORF204	235379	236689	putative				
ORF205	236680	237618	putative				
ORF206	237521	238345	putative				
ORF207	238281	238973	putative				
ORF208	238871	240115	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF209	240191	241564	putative				
ORF210	242281	241604	YqjZ	D84432	<i>Bacillus subtilis</i>	379	39
ORF211	242933	242274	f222; This 222 aa orf is 48 pct identical (0 gaps) to 208 residues of an approx. 232 aa protein YCKA BACSU SW: P42399	AE000284	<i>Escherichia coli</i>	382	45
ORF212	243416	242976	arginine repressor protein (argR)	U32800	<i>Haemophilus influenzae</i>	229	46
ORF213	243500	244531	sialoglycoprotease	U15958	<i>Pasteurella haemolytica</i>	565	53
ORF214	244480	246021	oligopeptide permease homolog AII	AF000366	<i>Borrelia burgdorferi</i>	457	34
ORF215	246330	247811	OppAIV	AF000948	<i>Borrelia burgdorferi</i>	453	35
ORF216	247831	249174	OppA gene product	X56347	<i>Bacillus subtilis</i>	255	37
ORF217	249437	251038	dcIAE	X56678	<i>Bacillus subtilis</i>	469	37
ORF218	251325	252212	OppB gene product	X56347	<i>Bacillus subtilis</i>	652	42
ORF219	253156	254007	oligopeptidase	X89237	<i>Streptococcus pyogenes</i>	574	48
ORF220	253974	254852	ATP binding protein	L18760	<i>Lactococcus lactis</i>	433	40
ORF221	255258	256094	KDO-transferase	X80061	<i>Chlamydia psittaci</i>	106	46
ORF222	256640	257455	putative				
ORF223	257502	258239	2-OXOGLUTARAT	A47930	<i>Spinacia oleracea</i>	636	52
ORF224	257869	257501	putative				
ORF225	259248	260897	pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta-subunit	M55191	<i>Solanum tuberosum</i>	1055	44
ORF226	262753	261788	putative				
ORF227	263059	262757	putative				
ORF228	264375	263182	putative				
ORF229	265985	264747	putative				
ORF230	266637	266059	putative				
ORF231	267338	266538	putative				
ORF232	267922	267473	putative				
ORF233	269647	270771	tRNA guanine transglycosylase	L33777	<i>Zymomonas mobilis</i>	628	44
ORF234	272777	273145	ORF 4	D00624	<i>Bacteriophage chp1</i>	100	41
ORF235	273253	273636	putative				
ORF236	273705	273977	putative				
ORF237	276016	275717	putative				
ORF238	276439	276020	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF239	276792	277253	putative				
ORF240	277318	277599	putative				
ORF241	278578	277877	putative				
ORF242	279258	278554	FbpC	U33937	<i>Neisseria gonorrhoeae</i>	312	39
ORF243	280435	279533	putative				
ORF244	281547	280849	putative				
ORF245	281696	282325	CMP-2-keto-3-deoxyoctulosonic acid synthetase	U15192	<i>Chlamydia trachomatis</i>	637	63
ORF246	282459	284069	CTP synthetase	U15192	<i>Chlamydia trachomatis</i>	2000	68
ORF247	284056	284517	ORF3	U15192	<i>Chlamydia trachomatis</i>	453	65
ORF248	284606	285775	glucose 6-phosphate dehydrogenase	U83195	<i>Chlamydia trachomatis</i>	1263	77
ORF249	285592	285987	glucose 6-phosphate dehydrogenase	U83195	<i>Chlamydia trachomatis</i>	519	79
ORF250	286179	286976	glucose-6-phosphate dehydrogenase isozyme	D88189	<i>Actinobacillus actinomycetemcomitans</i>	216	40
ORF251	287583	287002	putative				
ORF252	287951	287451	putative				
ORF253	288499	288816	putative				
ORF254	289674	288505	putative				
ORF255	288839	289213	putative				
ORF256	289970	290254	putative				
ORF257	291931	292803	gamma-D-glutamyl-L-diamino acid endopeptidase II	X64809	<i>Bacillus sphaericus</i>	95	39
ORF258	293258	292755	ScoS9	U43429	<i>Streptomyces coelicolor</i>	233	45
ORF259	293718	293272	ribosomal protein L13 (rpL13)	U32823	<i>Haemophilus influenzae</i>	364	47
ORF260	294630	293953	glutamine transport ATP-binding protein Q	U67524	<i>Methanococcus jannaschii</i>	387	46
ORF261	296153	294636	putative				
ORF262	294817	295068	putative				
ORF263	296354	297862	conserved hypothetical protein	AE000586	<i>Helicobacter pylori</i>	641	46
ORF264	298415	297879	putative				
ORF265	298777	298253	putative				
ORF266	299572	298781	putative				
ORF267	300487	299633	putative				
ORF268	301586	300702	putative				



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF269	302440	301571	putative				
ORF270	302838	302437	putative				
ORF271	303335	302745	putative				
ORF272	304394	303852	putative				
ORF273	304606	305223	f311; This 311 aa orf is 22 pct identical (13 gaps) to 186 residues of an approx. 488 aa protein YACA_BACSU SW: P37563; pyul of D21139	AE000232	<i>Escherichia coli</i>	250	38
ORF274	305394	306236	survival protein surE	U81296	<i>Sinorhizobium meliloti</i>	156	42
ORF275	306501	307439	YqfU	D84432	<i>Bacillus subtilis</i>	547	42
ORF276	308033	307458	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	U61168	<i>Bacillus firmus</i>	403	42
ORF277	308924	308037	4-hydroxybenzoate octaprenyltransferase	U61168	<i>Bacillus firmus</i>	152	40
ORF278	309485	310180	putative				
ORF279	310426	311214	putative				
ORF280	311597	311253	putative				
ORF281	312772	311780	putative				
ORF282	313425	312772	putative				
ORF283	313646	313377	putative				
ORF284	313937	314665	lysophospholipase homolog	AF006678	<i>Schistosoma mansoni</i>	141	44
ORF285	315576	314755	dnaZX	X17014	<i>Bacillus subtilis</i>	154	39
ORF286	316157	315531	unknown	D26185	<i>Bacillus subtilis</i>	284	31
ORF287	318657	316156	DNA gyrase	L47978	<i>Aeromonas salmonicida</i>	1785	48
ORF288	321042	318676	DNA gyrase subunit B	U35453	<i>Clostridium acetobutylicum</i>	1838	59
ORF289	321445	321098	putative				
ORF290	322309	321710	putative				
ORF291	323190	322366	outer membrane protein	AE000654	<i>Helicobacter pylori</i>	376	43
ORF292	323843	323181	hypothetical	U70214	<i>Escherichia coli</i>	356	37
ORF293	324878	323856	ATP-binding protein (abc)	U32744	<i>Haemophilus influenzae</i>	545	44
ORF294	325340	326410	f374; This 374 aa orf is 30 pct identical (9 gaps) to 102 residues of an approx. 512 aa protein FLIC SALMU SW: P06177	AE000299	<i>Escherichia coli</i>	1194	62
ORF295	326433	327836	Xas A	AE000246	<i>Escherichia coli</i>	479	33



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF296	328465	327839	putative				
ORF297	329360	328857	putative				
ORF298	330907	329357	putative				
ORF299	332455	330956	MgtE	U18744	<i>Bacillus firmus</i>	203	36
ORF300	334536	332395	putative				
ORF301	336091	334877	putative				
ORF302	336103	337302	putative				
ORF303	338129	338830	putative				
ORF304	338965	339501	putative				
ORF305	339508	340143	putative				
ORF306	340247	342967	putative				
ORF307	343385	343810	cAMP-dependent protein kinase type I regulatory subunit	U75932	<i>Rattus norvegicus</i>	102	37
ORF308	344171	343935	acyl carrier protein (acpP)	AE000570	<i>Helicobacter pylori</i>	198	55
ORF309	345082	344330	3-ketoacyl-ACP reductase	U39441	<i>Vibrio harveyi</i>	598	48
ORF310	346005	345082	malonyl-CoA:Acyl carrier protein transacylase	U59433	<i>Bacillus subtilis</i>	538	45
ORF311	346784	346437	beta-ketoacyl-acyl carrier protein synthase III (fabH)	AE000540	<i>Helicobacter pylori</i>	273	50
ORF312	347029	346715	beta-ketoacyl-acyl carrier protein synthase III	M77744	<i>Escherichia coli</i>	265	63
ORF313	347034	347723	recombination protein	D90916	<i>Synechocystis sp.</i>	363	42
ORF314	348075	350459	putative				
ORF315	350598	351071	putative				
ORF316	351075	352175	rifampicin resistance protein	L22690	<i>Rickettsia rickettsii</i>	495	46
ORF317	353291	352230	putative				
ORF318	353442	354467	pyruvate dehydrogenase E1 component, alpha subunit	D90915	<i>Synechocystis sp.</i>	571	44
ORF319	354451	354933	pyruvate dehydrogenase E1 beta subunit	U09137	<i>Arabidopsis thaliana</i>	495	59
ORF320	355000	355449	pyruvate dehydrogenase E1 component, beta subunit	U38804	<i>Porphyra purpurea</i>	336	47
ORF321	355448	356743	F23B12.5	Z77659	<i>Caenorhabditis elegans</i>	759	46
ORF322	355953	355642	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF323	359310	356827	glycogen phosphorylase B	U47025	<i>Homo sapiens</i>	2193	57
ORF324	359120	359377	putative				
ORF325	359525	359908	putative				
ORF326	361290	359947	DnaA	D89066	<i>Staphylococcus aureus</i>	375	46
ORF327	363785	361362	hypothetical	U32781	<i>Haemophilus influenzae</i>	394	44
ORF328	364496	363888	putative				
ORF329	364832	365290	putative				
ORF330	365304	365669	dpi	M76470	<i>Escherichia coli</i>	160	45
ORF331	366599	365667	NADPH thioredoxin reductase	AC002329	<i>Arabidopsis thaliana</i>	975	60
ORF332	367291	369030	ribosomal protein S1 (rpS1)	U32801	<i>Haemophilus influenzae</i>	1209	41
ORF333	369134	369808	NusA	U74759	<i>Chlamydia trachomatis</i>	995	87
ORF334	369917	370438	NusA	U74759	<i>Chlamydia trachomatis</i>	760	87
ORF335	370365	372647		U74759	<i>Chlamydia trachomatis</i>	2173	61
ORF336	372557	373066	initiation factor IF2-beta (infB; gtg start codon)	X00513	<i>Escherichia coli</i>	333	39
ORF337	373020	373442	ORF6 gene product	Z18631	<i>Bacillus subtilis</i>	192	34
ORF338	373467	374195	tRNA pseudouridine 5S synthase	D90917	<i>Synechocystis sp.</i>	358	47
ORF339	374176	375099	hypothetical 34.6 kD protein in rpsT-ileS intergenic region	AE000113	<i>Escherichia coli</i>	395	39
ORF340	375676	375083	hypothetical GTP-binding protein in pth 3' region	AE000219	<i>Escherichia coli</i>	507	53
ORF341	376173	375634	hypothetical	U32723	<i>Haemophilus influenzae</i>	480	59
ORF342	376564	377643	YscU	U08019	<i>Yersinia enterocolitica</i>	538	37
ORF343	377956	379773	lcrD gene product	X67771	<i>Yersinia enterocolitica</i>	1302	47
ORF344	379781	380425	putative				
ORF345	380281	381000	putative				
ORF346	381008	381460	putative				
ORF347	381460	383037	4-alpha-glucanotransferase	L37874	<i>Clostridium butyricum</i>	302	38
ORF348	383257	383523	ribosomal protein L28 (rpL28)	U32776	<i>Haemophilus influenzae</i>	175	55
ORF349	383553	385304	hypothetical protein	D90901	<i>Synechocystis sp.</i>	565	38
ORF350	385397	386458	comE ORF1	D64002	<i>Synechocystis sp.</i>	187	10
ORF351	387242	386514	putative				
ORF352	388764	387013	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF353	390120	390932	methylentetrahydrofolate dehydrogenase	D64000	<i>Synechocystis</i> sp.	588	53
ORF354	390919	391818	f351; Residues 1-121 are 100 pct identical to YOJL_ECOLI SW: P33944 (122 aa) and aa 152-351 are 100 pct identical to YOJK_ECOLI SW: P33943	AE000310	<i>Escherichia coli</i>	186	39
ORF355	392379	391885	small protein	D90914	<i>Synechocystis</i> sp.	387	46
ORF356	392582	392986	putative				
ORF357	392776	393684	putative				
ORF358	394151	394804	RecF protein	D90907	<i>Synechocystis</i> sp.	232	34
ORF359	394928	395308	putative				
ORF360	395259	395990	putative				
ORF361	397815	395953	hypothetical	U32773	<i>Haemophilus influenzae</i>	391	36
ORF362	398850	397831	H. influenzae predicted coding region HI0807	U32763	<i>Haemophilus influenzae</i>	580	39
ORF363	400085	399099	putative				
ORF364	401245	400073	YtgC	AF008220	<i>Bacillus subtilis</i>	244	30
ORF365	401474	401136	putative				
ORF366	402199	401423	unknown	U52850	<i>Erysipelothrix rhusiopathiae</i>	534	46
ORF367	403193	402186	putative				
ORF368	403650	404165	putative				
ORF369	404343	405914	adenine nucleotide translocase	Z49227	<i>Arabidopsis thaliana</i>	1280	55
ORF370	405984	407327	putative				
ORF371	407712	408806	putative				
ORF372	410439	409075	putative				
ORF373	411826	410954	putative				
ORF374	412482	414302	lepA gene product	X91655	<i>Bacillus subtilis</i>	1827	59
ORF375	415402	414407	6-phosphogluconate dehydrogenase, decarboxylating (gnd)	U32737	<i>Haemophilus influenzae</i>	687	51
ORF376	415848	415237	6-phosphogluconate dehydrogenase, 6PGD [Ceratitis capitata=medflies, Peptide, 481 aa]	S67873	<i>Ceratitis capitata</i>	695	64
ORF377	417131	415866	tyrosyl-tRNA synthetase (tyrS)	J01719	<i>Escherichia coli</i>	821	45
ORF378	417258	417566	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF379	418326	417454	whiG-Stv gene product	X68709	<i>Streptovorticillium griseocarneum</i>	464	41
ORF380	420057	418426	FLHA gene product	X63698	<i>Bacillus subtilis</i>	455	49
ORF381	420448	420720	ferredoxin IV	M59855	<i>Rhodobacter capsulatus</i>	174	63
ORF382	420980	421552	putative				
ORF383	421556	422029	putative				
ORF384	422461	422925	putative				
ORF385	423562	424320	putative				
ORF386	424250	424591	putative				
ORF387	424830	426047	putative				
ORF388	426240	427397	putative				
ORF389	428841	430703	GcpE	D90908	<i>Synechocystis sp.</i>	877	47
ORF390	430694	431446	YfiH	U50134	<i>Escherichia coli</i>	136	35
ORF391	431597	432100	putative				
ORF392	432165	432779	putative				
ORF393	433272	432832	dihydrolipoamide succinyltransferase (sucB)	U32839	<i>Haemophilus influenzae</i>	475	64
ORF394	433925	433227	dihydrolipoamide succinyltransferase (sucB)	U32839	<i>Haemophilus influenzae</i>	332	45
ORF395	436678	433934	alpha-ketoglutarate dehydrogenase	U41762	<i>Rhodobacter capsulatus</i>	1530	44
ORF396	437176	438357	oxygen-independent coproporphyrinogen III oxidase (hemN)	AE000628	<i>Helicobacter pylori</i>	442	42
ORF397	440317	438518	putative				
ORF398	440001	440345	putative				
ORF399	441233	440517	ORF f286	U18997	<i>Escherichia coli</i>	168	45
ORF400	440719	441012	putative				
ORF401	442192	441230	putative				
ORF402	442888	442343	putative				
ORF403	442371	442961	putative				
ORF404	443578	443003	[karp] gene products	M86605	<i>Chlamydia trachomatis</i>	505	78
ORF405	444500	443526	aminopeptidase	D17450	<i>Mycoplasma salivarium</i>	273	39
ORF406	444842	444528	putative				
ORF407	445009	444743	putative	L39923	<i>Mycobacterium leprae</i>	133	33

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF408	445718	445182	putative				
ORF409	445807	447804	Sulp	U18908	<i>Zea mays</i>	1307	52
ORF410	448738	447803	putative				
ORF411	449628	448618	RuvB protein	U38840	<i>Thermotoga maritima</i>	845	53
ORF412	450298	450867	deoxycytidine triphosphate deaminase (dcd)	AE000554	<i>Helicobacter pylori</i>	573	58
ORF413	450713	451207	putative				
ORF414	451211	452452	hemolysin	D90914	<i>Synechocystis sp.</i>	227	39
ORF415	452448	453659	similar to [SwissProt Accession Number P37908]	D90888	<i>Escherichia coli</i>	96	33
ORF416	454843	453725	NiS gene product	L34879	<i>Anabaena azollae</i>	533	38
ORF417	455608	454865	hypothetical protein	D90908	<i>Synechocystis sp.</i>	371	36
ORF418	456243	457007	putative				
ORF419	457016	457708	putative				
ORF420	458368	457979	unknown	D26185	<i>Bacillus subtilis</i>	152	36
ORF421	459496	458372	mutY homolog	U63329	<i>Homo sapiens</i>	466	46
ORF422	459493	460194	hypothetical protein	D90914	<i>Synechocystis sp.</i>	98	38
ORF423	461446	460355	putative				
ORF424	462298	461450	putative				
ORF425	462444	463349	enoyl-ACP reductase	Y13861	<i>Nicotiana tabacum</i>	1008	69
ORF426	464241	463342	putative				
ORF427	464574	465065	putative				
ORF428	465129	465611	putative				
ORF429	465571	466317	putative				
ORF430	466317	467093	H. pylori predicted coding region HP0152	AE000536	<i>Helicobacter pylori</i>	246	36
ORF431	466999	467502	putative				
ORF432	469691	467715	unidentified transporter-ATP binding	Z82044	<i>Bacillus subtilis</i>	496	45
ORF433	470691	469660	acetyl-CoA carboxylase subunit	AF008220	<i>Bacillus subtilis</i>	781	52
ORF434	472010	470709	putative				
ORF435	471545	471799	putative				
ORF436	472359	472045	putative				
ORF437	473523	472732	orf1	X75413	<i>Escherichia coli</i>	313	42
ORF438	474889	473441	murE gene product	Z15056	<i>Bacillus subtilis</i>	679	37
ORF439	477323	475365	penicillin-binding protein 2	X59630	<i>Neisseria meningitidis</i>	451	42

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF440	478496	477597	hypothetical protein	D90906	<i>Synechocystis sp.</i>	534	52
ORF441	478722	479273	putative				
ORF442	479277	479705	putative				
ORF443	480050	481450	chromosomal replication initiator protein	D90909	<i>Synechocystis sp.</i>	793	40
			DnaA				
ORF444	481469	482053	OrfH	U35673	<i>Borrelia burgdorferi</i>	157	37
ORF445	482600	482025	putative				
ORF446	482654	484204	NADH:ubiquinone oxidoreductase subunit B	Z37111	<i>Vibrio alginolyticus</i>	801	49
ORF447	484211	485170	NADH:ubiquinone oxidoreductase (GP:Z37111 4)	U32702	<i>Haemophilus influenzae</i>	258	48
ORF448	485170	485838	NADH:ubiquinone oxidoreductase	Z37111	<i>Vibrio alginolyticus</i>	543	55
ORF449	485813	486580	unidentified protein of Na <sup>+</sup> -translocating NADH-quinone reductase	D49364	<i>Vibrio alginolyticus</i>	488	48
ORF450	486976	486638	putative				
ORF451	489071	487764	putative				
ORF452	489341	489090	putative				
ORF453	489958	489152	putative				
ORF454	490549	489962	putative				
ORF455	491163	490522	putative				
ORF456	491396	491112	putative				
ORF457	492121	491390	putative				
ORF458	492304	494838	ClpC adenosine triphosphatase	U02604	<i>Bacillus subtilis</i>	2370	46
ORF459	495943	494822	hypothetical protein in purB 5' region	AE000213	<i>Escherichia coli</i>	927	53
ORF460	496011	496565	putative				
ORF461	496569	497228	putative				
ORF462	497358	497834	putative				
ORF463	497770	498327	putative				
ORF464	499209	499589	putative				
ORF465	499520	499792	putative				
ORF466	500774	504169	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1215	45
ORF467	504139	504600	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	319	47
ORF468	504865	506877	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	992	42

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF469	506790	507671	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	739	46
ORF470	507718	510507	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1813	42
ORF471	508325	507912	putative				
ORF472	510660	513440	POMP90A precursor	U65942	<i>Chlamydia psittaci</i>	1830	46
ORF473	514965	513787	hypothetical	D83026	<i>Bacillus subtilis</i>	482	48
ORF474	517347	515419	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1554	51
ORF475	517058	517363	putative				
ORF476	517798	517277	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	222	41
ORF477	518200	517847	POMP91B precursor	U65943	<i>Chlamydia psittaci</i>	162	42
ORF478	518300	521146	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1900	45
ORF479	521392	522948	POMP91A	U65942	<i>Chlamydia psittaci</i>	490	39
ORF480	523244	524809	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	507	35
ORF481	524379	524125	putative				
ORF482	524649	526238	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	969	41
ORF483	526265	527104	putative				
ORF484	526947	526702	putative				
ORF485	526975	528450	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	197	48
ORF486	528408	529199	putative outer membrane protein	U72499	<i>Chlamydia psittaci</i>	154	37
ORF487	530612	529542	putative				
ORF488	531656	530616	putative				
ORF489	533974	532067	putative				
ORF490	536432	534324	putative				
ORF491	537150	536707	putative				
ORF492	537928	537080	putative				
ORF493	538438	537932	putative				
ORF494	538737	538333	putative				
ORF495	539594	539127	putative				
ORF496	541215	539590	putative				
ORF497	542571	541282	putative				
ORF498	543014	542457	putative				
ORF499	543369	542962	putative				
ORF500	543809	546628	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	506	89
ORF501	546619	549525	POMP91A	U65942	<i>Chlamydia psittaci</i>	128	50



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF502	547293	546994	putative				
ORF503	549699	550523	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	96	32
ORF504	550490	551551	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	223	33
ORF505	551448	552623	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	139	46
ORF506	552652	555117	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	487	48
ORF507	555029	555493	putative				
ORF508	558006	555673	putative				
ORF509	559694	558162	putative				
ORF510	558208	558573	putative				
ORF511	561692	559899	putative				
ORF512	561412	561708	putative				
ORF513	563942	561777	1,4-alpha-glucan branching enzyme	X73903	<i>Streptomyces coelicolor</i>	1743	45
ORF514	564969	563950	putative				
ORF515	566204	564936	YqeV	D84432	<i>Bacillus subtilis</i>	639	38
ORF516	567717	566302	putative GTPase required for high frequency lysogenization by bacteriophage lambda	U00005	<i>Escherichia coli</i>	686	41
ORF517	568526	567708	putative				
ORF518	569467	568742	putative				
ORF519	571065	569431	putative				
ORF520	571828	571118	arginine-binding periplasmic protein 1 precursor	AE000188	<i>Escherichia coli</i>	197	45
ORF521	572202	573308	putative				
ORF522	573146	575056	putative				
ORF523	575023	575916	carboxysome formation protein	D90901	<i>Synechocystis sp.</i>	557	59
ORF524	577891	576497	putative				
ORF525	578914	578204	putative				
ORF526	579924	578857	putative				
ORF527	580187	579858	protein kinase C inhibitor	D90906	<i>Synechocystis sp.</i>	260	49
ORF528	580017	580406	putative				
ORF529	581086	580187	Yer156cp	U18917	<i>Saccharomyces cerevisiae</i>	176	34
ORF530	581367	581828	putative				
ORF531	581678	582367	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF532	582361	583428	putative				
ORF533	584690	583431	putative				
ORF534	585237	584950	putative				
ORF535	585626	586888	hypothetical protein	D64004	<i>Synechocystis sp.</i>	805	45
ORF536	586846	587907	putative				
ORF537	589049	588180	putative				
ORF538	590500	589301	putative				
ORF539	590755	592458	aminoacyl-tRNA synthetase	L25105	<i>Chlamydia trachomatis</i>	2125	71
ORF540	592526	592903	has homology to putative heat shock proteins of <i>Bacillus subtilis</i> and <i>Clostridium acetobutylicum</i> ; ORFA: putative	L25105	<i>Chlamydia trachomatis</i>	324	59
ORF541	592836	593747	Possible negative regulator of CIRCE element; Homologs in <i>B. subtilis</i> and <i>Clostridia</i> spp. referred to as hrcA or orfA	U52216	<i>Chlamydia trachomatis</i>	960	65
ORF542	593747	594298	grpE	M62819	<i>Chlamydia trachomatis</i>	661	71
ORF543	594331	595947	DnaK protein homolog; 71,550 Da; putative	M69227	<i>Chlamydia pneumoniae</i>	2619	100
ORF544	595905	596309	DnaK protein homolog; 71,550 Da; putative	M69227	<i>Chlamydia pneumoniae</i>	674	100
ORF545	596514	597215	putative				
ORF546	597184	597957	vacB gene product	U14003	<i>Escherichia coli</i>	306	48
ORF547	597755	598612	ORF-2	D11024	<i>Shigella flexneri</i>	168	46
ORF548	598602	599204	homologous to DNA glycosylases; hypothetical	D83026	<i>Bacillus subtilis</i>	374	47
ORF549	599373	599939	putative				
ORF550	600903	602072	hemolysin	X73141	<i>Serpulina hyodysenteriae</i>	362	36
ORF551	602240	602587	hypothetical protein	D90908	<i>Synechocystis sp.</i>	182	35
ORF552	602637	603272	putative				
ORF553	603142	604512	putative				
ORF554	604627	605853	conserved hypothetical protein	AE000579	<i>Helicobacter pylori</i>	423	40
ORF555	605790	606620	putative				
ORF556	606571	607281	putative	L14679	<i>Lactococcus lactis</i>	384	45
ORF557	609004	607355	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF558	610906	609932	putative				
ORF559	611786	611004	diaminopimelate epimerase	D90917	<i>Synechocystis</i> sp.	207	55
ORF560	612333	611746	ATP-dependent Clp protease proteolytic subunit	D90915	<i>Synechocystis</i> sp.	389	44
ORF561	613897	612341	serine hydroxymethyltransferase	D90903	<i>Synechocystis</i> sp.	909	52
ORF562	615179	616279	putative				
ORF563	616610	617383	putative				
ORF564	618796	617810	ORF 0328	U18997	<i>Escherichia coli</i>	413	45
ORF565	620004	618826	branched chain alpha-keto acid dehydrogenase E2	M97391	<i>Bacillus subtilis</i>	688	41
ORF566	619649	619918	putative				
ORF567	621265	620021	Hypothetical protein	Y14083	<i>Bacillus subtilis</i>	727	37
ORF568	622359	621265	hypothetical	U32691	<i>Haemophilus influenzae</i>	294	52
ORF569	623420	622560	rRNA methylase	D90913	<i>Synechocystis</i> sp.	244	38
ORF570	624297	623335	hypothetical protein (SP:P39587)	U67605	<i>Methanococcus jannaschii</i>	147	35
ORF571	624773	624174	riboflavin synthase alpha chain	AE000261	<i>Escherichia coli</i>	424	50
ORF572	625029	625484	ORF 168	D28752	<i>Synechococcus</i> sp.	323	43
ORF573	625488	625883	YteA	AF008220	<i>Bacillus subtilis</i>	172	35
ORF574	625892	626395	signalpeptidase II	X78084	<i>Staphylococcus carnosus</i>	204	38
ORF575	626444	627790	D-alanine permease (dagA)	U32770	<i>Haemophilus influenzae</i>	566	33
ORF576	627912	628607	putative				
ORF577	628774	629697	putative				
ORF578	629660	631639	POMP91A	U65942	<i>Chlamydia psittaci</i>	579	44
ORF579	631725	633551	putative				
ORF580	633520	636957	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	266	45
ORF581	637232	638098	adhesion protein	D90903	<i>Synechocystis</i> sp.	267	38
ORF582	640648	639593	GTP-binding protein	D90901	<i>Synechocystis</i> sp.	759	45
ORF583	640979	640728	50S ribosomal protein L27	U38804	<i>Porphyra purpurea</i>	265	65
ORF584	641327	641007	50S ribosomal subunit protein L21	U18997	<i>Escherichia coli</i>	210	41
ORF585	641687	642283	hypothetical protein	D90906	<i>Synechocystis</i> sp.	76	39
ORF586	643023	642286	assimilatory sulfite reductase	L26503	<i>Saccharomyces cerevisiae</i>	284	42
ORF587	643330	643076	putative				
ORF588	643704	643351	ribosomal protein S10 (rpS10)	U32761	<i>Haemophilus influenzae</i>	349	69

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF589	645628	643676	translation elongation factor EF-G (fusA)	AE000625	<i>Helicobacter pylori</i>	1991	58
ORF590	645783	645538	elongation factor G (AA 1-691)	X16278	<i>Thermus aquaticus thermophilus</i>	170	80
ORF591	646269	645793	ribosomal protein S7	Z11567	<i>Chlamydia trachomatis</i>	730	88
ORF592	646751	646314	ribosomal protein S12 (AA 1-123)	X52912	<i>Cryptomonas phi</i>	485	67
ORF593	647848	647045	putative				
ORF594	648393	650336	ORF of prc gene (alt.)	D00674	<i>Escherichia coli</i>	554	42
ORF595	651016	650420	hypothetical sulfur-rich protein	U41759	<i>Chlamydia psittaci</i>	301	50
ORF596	652956	651289	60kDa CrP	X53511	<i>Chlamydia pneumoniae</i>	2951	100
ORF597	653395	653126	9kDa CrP	X53511	<i>Chlamydia pneumoniae</i>	502	99
ORF598	655740	654193	glutamyl-tRNA synthetase homolog	U41759	<i>Chlamydia psittaci</i>	2259	82
ORF599	656508	655966	early stage-specific transcription experimentally demonstrated; early upstream open reading frame (EUO)	L13598	<i>Chlamydia psittaci</i>	666	62
ORF600	658140	657022	unknown	U41759	<i>Chlamydia psittaci</i>	950	44
ORF601	660216	658525	RecJ recombination protein	U41759	<i>Chlamydia psittaci</i>	807	73
ORF602	663238	660248	protein-export membrane protein SecD	D64000	<i>Synechocystis sp.</i>	413	41
ORF603	664461	663157	putative				
ORF604	665735	664635	putative				
ORF605	666212	666994	hypothetical protein	D64006	<i>Synechocystis sp.</i>	538	58
ORF606	666998	667921	o298; This 298 aa orf is 33 pct identical (24 gaps) to 248 residues of an approx. 256 aa protein CDSA ECOLI SW: P06466	AE000238	<i>Escherichia coli</i>	253	45
ORF607	667909	668568	cytidylate kinase	AE000193	<i>Escherichia coli</i>	400	48
ORF608	668502	669203	hypothetical protein	D90915	<i>Synechocystis sp.</i>	225	33
ORF609	669154	670893	arginyl-tRNA-synthetase	D64006	<i>Synechocystis sp.</i>	1365	49
ORF610	672226	670853	UDP-N-acetylglucosamine enolpyruvyl transferase (murZ)	U32788	<i>Haemophilus influenzae</i>	642	40
ORF611	671137	671424	putative				
ORF612	672453	673001	putative				
ORF613	673072	674721	putative				
ORF614	674549	674262	putative				
ORF615	675518	674796	ORF246 gene product	X59551	<i>Escherichia coli</i>	520	43
ORF616	676083	675499	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF617	676630	676067	putative				
ORF618	677016	676600	ORF3	D10279	<i>Bacillus subtilis</i>	361	63
ORF619	677647	677015	peptide release factor 2	X99401	<i>Bacillus firmus</i>	427	43
ORF620	677990	678259	unknown	Z49939	<i>Saccharomyces cerevisiae</i>	175	48
ORF621	679444	680097	unknown	D26185	<i>Bacillus subtilis</i>	263	38
ORF622	680097	680897	unknown	D64126	<i>Bacillus subtilis</i>	506	45
ORF623	681637	680849	putative				
ORF624	681409	682281	putative				
ORF625	682453	682821	putative				
ORF626	682763	683902	sensor protein	L39904	<i>Myxococcus xanthus</i>	190	48
ORF627	684616	683969	putative				
ORF628	685169	684534	putative				
ORF629	685986	685117	putative				
ORF630	686278	687288	NtrC/NifA-like protein regulator	U17902	<i>Escherichia coli</i>	820	45
ORF631	687483	688151	putative				
ORF632	688740	689501	putative				
ORF633	690242	689622	putative				
ORF634	690470	691126	unknown	Z48008	<i>Saccharomyces cerevisiae</i>	380	46
ORF635	692600	691497	putative				
ORF636	692674	695064	phenylalanyl-tRNA synthetase beta-subunit (pheT)	U32810	<i>Haemophilus influenzae</i>	593	45
ORF637	695049	696032	putative				
ORF638	697964	696585	OppC-like protein	D85103	<i>Synechococcus sp.</i>	371	37
ORF639	699803	698274	OppB gene product	X56347	<i>Bacillus subtilis</i>	197	40
ORF640	701926	699788	AppA	U20909	<i>Bacillus subtilis</i>	324	43
ORF641	703196	702567	putative				
ORF642	704221	703208	putative				
ORF643	704240	705289	ferrochelatase	X73417	<i>Arabidopsis thaliana</i>	266	42
ORF644	706070	705300	histidine periplasmic binding protein P29	U58045	<i>Campylobacter jejuni</i>	128	31
ORF645	706841	706254	conserved hypothetical protein	AE000592	<i>Helicobacter pylori</i>	155	37
ORF646	707596	706811	putative				
ORF647	708666	707677	ADP-glucose pyrophosphorylase	X55650	<i>Solanum tuberosum</i>	595	43
ORF648	709793	709119	pyrE-F gene product	X71842	<i>Arabidopsis thaliana</i>	400	44

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF649	711523	710132	transcription termination factor	J01673	<i>Escherichia coli</i>	1251	60
ORF650	712236	711523	putative				
ORF651	714734	712125	DNA polymerase I	J04479	<i>Streptococcus pneumoniae</i>	1334	43
ORF652	715759	714761	protease IV	U67512	<i>Methanococcus jannaschii</i>	101	55
ORF653	717538	715886	adenine nucleotide translocase	Z49227	<i>Arabidopsis thaliana</i>	832	39
ORF654	719113	720243	replicative DNA helicase	D26185	<i>Bacillus subtilis</i>	776	44
ORF655	720590	722422	homologous to E.coli gidA	X62540	<i>Pseudomonas putida</i>	1575	52
ORF656	722406	723056	putative				
ORF657	723551	723120	nucleoside 5'-diphosphate phosphotransferase (EC 2.7.4.6)	J05207	<i>Myxococcus xanthus</i>	451	62
ORF658	724246	723626	Holliday junction DNA helicase (ruvA)	U32716	<i>Haemophilus influenzae</i>	293	43
ORF659	724754	724251	crossover junction endodeoxyribonuclease (ruvC)	U32717	<i>Haemophilus influenzae</i>	296	53
ORF660	725868	724900	putative				
ORF661	727115	726270	putative				
ORF662	728126	727119	glyceraldehyde-3-phosphate dehydrogenase	U83198	<i>Chlamydia trachomatis</i>	1340	75
ORF663	728594	728208	ribosomal protein L17	L33834	<i>Chlamydia trachomatis</i>	439	82
ORF664	729614	728604	RNA polymerase alpha-subunit	L33834	<i>Chlamydia trachomatis</i>	1356	89
ORF665	729778	729533	RNA polymerase alpha-subunit	L33834	<i>Chlamydia trachomatis</i>	273	82
ORF666	730149	729751	ribosomal protein S11	L33834	<i>Chlamydia trachomatis</i>	562	90
ORF667	730539	730174	ribosomal protein S13	L33834	<i>Chlamydia trachomatis</i>	544	89
ORF668	731983	730598	homolog	L25077	<i>Chlamydia trachomatis</i>	1956	83
ORF669	732427	731996	ribosomal protein CtrL15e	M80325	<i>Chlamydia trachomatis</i>	563	77
ORF670	732917	732423	ribosomal protein CtrS5e	M80325	<i>Chlamydia trachomatis</i>	702	84
ORF671	733598	733320	ribosomal protein L6	M60652	<i>Chlamydia trachomatis</i>	316	87
ORF672	733869	733492	ribosomal protein L6	M60652	<i>Chlamydia trachomatis</i>	469	77
ORF673	734298	733900	ribosomal protein CtrS8e	M80325	<i>Chlamydia trachomatis</i>	572	82
ORF674	734858	734319	ribosomal protein CtrL5e	M80325	<i>Chlamydia trachomatis</i>	730	90
ORF675	735195	734863	ribosomal protein CtrL24e	M80325	<i>Chlamydia trachomatis</i>	420	70
ORF676	735578	735342	ribosomal protein CtrL14e	M80325	<i>Chlamydia trachomatis</i>	270	95
ORF677	735861	735604	ribosomal protein S17e	M80325	<i>Chlamydia trachomatis</i>	322	77
ORF678	736492	736079	50S ribosomal protein L16	D90905	<i>Synechocystis sp.</i>	439	60

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF679	737192	736524	ribosomal protein S3	D64071	<i>Actinobacillus actinomycetemcomitans</i>	612	58
ORF680	737555	737211	ribosomal protein L22	Z21677	<i>Thermotoga maritima</i>	228	48
ORF681	738688	737837	50S ribosomal subunit protein L2	U18997	<i>Escherichia coli</i>	769	62
ORF682	739048	738713	putative				
ORF683	739736	739065	ribosomal protein L4	X67014	<i>Bacillus stearothermophilus</i>	308	46
ORF684	740477	739773	ribosomal protein L3	Z46265	<i>Thermus aquaticus thermophilus</i>	463	50
ORF685	740659	740958	putative				
ORF686	741722	740721	putative				
ORF687	742789	741827	methionyl-tRNA formyltransferase	D64001	<i>Synechocystis sp.</i>	511	48
ORF688	743618	742782	UDP-N-acetylglucosamine acyltransferase	L22690	<i>Rickettsia rickettsii</i>	542	43
ORF689	744092	743634	(3R)-hydroxymyristol acyl carrier protein dehydrase	D90910	<i>Synechocystis sp.</i>	339	55
ORF690	744604	744107	UDP-3-O-acyl N-acetylglucosamine deacetylase	D90902	<i>Synechocystis sp.</i>	287	45
ORF691	744953	744498	UDP-3-O-acyl-GlcNAc deacetylase	U67855	<i>Pseudomonas aeruginosa</i>	262	51
ORF692	746608	744986	apolipoprotein N-acyltransferase (cute)	U32716	<i>Haemophilus influenzae</i>	194	50
ORF693	747085	746621	low homology to P14 protein of <i>Haemophilus influenzae</i> and 14.2 kDa protein of <i>Escherichia coli</i>	D78189	<i>Bacillus subtilis</i>	235	37
ORF694	747974	747219	polymerase III	M22996	<i>Bacillus subtilis</i>	180	34
ORF695	748594	748169	hypothetical protein	D90914	<i>Synechocystis sp.</i>	160	43
ORF696	749145	748573	putative				
ORF697	749652	749957	trxA	L39892	<i>Chlamydia psittaci</i>	393	72
ORF698	750446	749979	spoU	L39892	<i>Chlamydia psittaci</i>	559	72
ORF699	751219	750446	mip	L39892	<i>Chlamydia psittaci</i>	948	60
ORF700	753042	751291	aspartyl-tRNA synthetase	D90910	<i>Synechocystis sp.</i>	1347	47
ORF701	754309	753020	histidine--tRNA ligase	Z17214	<i>Streptococcus equisimilis</i>	757	44
ORF702	755120	756175	hexosephosphate transport protein	M89480	<i>Salmonella typhimurium</i>	870	49
ORF703	756120	756485	hexosephosphate transport protein	M89479	<i>Escherichia coli</i>	321	45
ORF704	756499	760227	DNA polymerase III alpha-subunit (dnaE)	AE000646	<i>Helicobacter pylori</i>	1977	42
ORF705	761217	760297	putative				
ORF706	761297	761809	putative				



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF707	761782	762282	putative				
ORF708	762260	762895	putative				
ORF709	762867	763316	hypothetical protein	D90908	<i>Synechocystis</i> sp.	177	43
ORF710	763780	763325	putative				
ORF711	763861	765168	DD-carboxypeptidase	M85047	<i>Bacillus subtilis</i>	292	37
ORF712	766809	765697	fmu and fmv protein	D90902	<i>Synechocystis</i> sp.	130	36
ORF713	768051	766888	putative				
ORF714	768566	768321	putative				
ORF715	769342	768551	putative				
ORF716	770532	769378	putative				
ORF717	771451	770804	putative				
ORF718	773058	771847	3-phosphoglycerate kinase	U83197	<i>Chlamydia trachomatis</i>	1540	72
ORF719	773094	773456	putative				
ORF720	774376	773093	putative phosphate permease	U84890	<i>Mesembryanthemum crystallinum</i>	870	45
ORF721	775123	774380	putative				
ORF722	775398	774916	putative				
ORF723	775046	776077	sporulation protein	M57689	<i>Bacillus subtilis</i>	698	43
ORF724	776070	777041	was dppE	U00039	<i>Escherichia coli</i>	565	56
ORF725	777964	777536	orf288; translated orf similarity to SWISS-PROT: YGI2_PSEPU hypothetical 32.4 kDa protein of <i>Pseudomonas putida</i>	Y10436	<i>Coxiella burnetii</i>	256	46
ORF726	778176	777904	B. subtilis genes rpmH, mpA, 50kd, gidA and gidB	X62539	<i>Bacillus subtilis</i>	112	37
ORF727	778621	779334	putative				
ORF728	781173	780307	f406; This 406 aa orf is 28 pct identical (12 gaps) to 264 residues of an approx. 440 aa protein YAOA_SCHPO SW: O10089	AE000263	<i>Escherichia coli</i>	603	40
ORF729	781526	781116	f406; This 406 aa orf is 28 pct identical (12 gaps) to 264 residues of an approx. 440 aa protein YAOA_SCHPO SW: O10089	AE000263	<i>Escherichia coli</i>	258	45
ORF730	782784	781555	f423; This 423 aa orf is 29 pct identical (1 gaps) to 172 residues of an approx. 488 aa protein YC24_CYAPA SW: P48260	AE000263	<i>Escherichia coli</i>	197	44

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF731	783572	782805	hypothetical chloroplast ORF 16	U38804	<i>Porphyrha purpurea</i>	597	52
ORF732	785032	783581	ABC transporter subunit	D64004	<i>Synechocystis sp.</i>	1720	62
ORF733	786412	785360	putative				
ORF734	788429	786450	pbp	Y14206	<i>Sireptomycetes coelicolor</i>	148	55
ORF735	788944	788528	penicillin-binding protein 3	X84053	<i>Pseudomonas aeruginosa</i>	148	38
ORF736	789758	788901	putative				
ORF737	790332	791504	major outer membrane protein	M64064	<i>Chlamydia pneumoniae</i>	2028	99
ORF738	791846	792721	ribosomal protein S2	U60196	<i>Chlamydia trachomatis</i>	904	70
ORF739	792724	793569	elongation factor Ts	U60196	<i>Chlamydia trachomatis</i>	1023	71
ORF740	793580	794323	UMP kinase	U60196	<i>Chlamydia trachomatis</i>	891	72
ORF741	794304	794843	ribosome-releasing factor	U60196	<i>Chlamydia trachomatis</i>	673	73
ORF742	795217	795732	unknown	D26185	<i>Bacillus subtilis</i>	105	42
ORF743	795722	796795	unknown	D26185	<i>Bacillus subtilis</i>	208	33
ORF744	798735	797053	putative	L33796	<i>Vibrio cholerae</i>	386	34
ORF745	799823	798681	putative				
ORF746	799297	799578	putative				
ORF747	801313	799808	Pkn5	U40656	<i>Myxococcus xanthus</i>	345	33
ORF748	802453	801332	putative				
ORF749	803299	802457	putative				
ORF750	803811	803290	putative				
ORF751	805151	803826	YscN	U02499	<i>Yersinia enterocolitica</i>	1185	53
ORF752	805860	805156	putative				
ORF753	806604	806332	putative				
ORF754	806913	806608	putative				
ORF755	808222	806903	putative				
ORF756	808751	808146	putative				
ORF757	809437	808673	putative				
ORF758	809939	809454	putative				
ORF759	811235	810213	delta-aminolevulinate synthase (EC 2.3.1.37)	M30785	<i>Escherichia coli</i>	172	40
ORF760	811779	813056	DNA gyrase subunit B	U35453	<i>Clostridium acetobutylicum</i>	584	38
ORF761	812890	812516	putative				
ORF762	812954	813583	DNA gyrase subunit B	Z19108	<i>Spiroplasma citri</i>	371	39

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF763	813587	815023	gyrA	X92503	<i>Mycobacterium smegmatis</i>	414	55
ORF764	815420	815746	putative				
ORF765	816036	817010	orf-X; hypothetical protein; Method: conceptual translation supplied by author	U48870	<i>Bacillus subtilis</i>	569	47
ORF766	817111	817356	unknown	Z74024	<i>Mycobacterium tuberculosis</i>	114	34
ORF767	817791	818609	3-deoxy-d-manno-octulosonic acid 8- phosphate synthetase	Z50747	<i>Chlamydia psittaci</i>	1112	78
ORF768	818609	819094	protein of unknown function	Z50747	<i>Chlamydia psittaci</i>	545	65
ORF769	819104	819823	ATP binding protein	U72493	<i>Chlamydia trachomatis</i>	1099	88
ORF770	820722	819826	putative				
ORF771	822313	821000	putative				
ORF772	823503	822238	putative				
ORF773	823678	825612	putative				
ORF774	825461	826312	putative				
ORF775	827280	826645	putative				
ORF776	828604	827171	76 kDa protein	L23921	<i>Chlamydia pneumoniae</i>	2179	100
ORF777	830026	828713	76 kDa protein	L23921	<i>Chlamydia pneumoniae</i>	1162	100
ORF778	831047	830085	mviB homolog	U50732	<i>Chlamydia trachomatis</i>	982	58
ORF779	831725	831051	mviB homolog	U50732	<i>Chlamydia trachomatis</i>	740	65
ORF780	832220	833098	T05H10.2	Z47812	<i>Caenorhabditis elegans</i>	407	34
ORF781	833851	833396	ribosomal protein S4 (rps4)	AE000633	<i>Helicobacter pylori</i>	372	53
ORF782	834068	835039	This ORF is homologous to a 40.0 kd hypothetical protein in the htrB 3' region from <i>E. coli</i> . Accession Number X61000	L22217	<i>Mycoplasma-like organism</i>	377	49
ORF783	835792	835127	uridine kinase	L31783	<i>Mus musculus</i>	436	43
ORF784	837624	836116	ORF f397	U29581	<i>Escherichia coli</i>	92	38
ORF785	838951	840882	putative				
ORF786	840869	842185	exodeoxyribonuclease V (recB)	U32811	<i>Haemophilus influenzae</i>	409	40
ORF787	841989	843455	DNA helicase II	U39703	<i>Mycoplasma genitalium</i>	110	46
ORF788	843242	844021	exodeoxyribonuclease V (recB)	U32811	<i>Haemophilus influenzae</i>	196	40
ORF789	845018	843987	MreC protein	M31792	<i>Escherichia coli</i>	76	53
ORF790	846174	844990	aspartate aminotransferase (aspC)	X03629	<i>Escherichia coli</i>	754	40
ORF791	848509	846311	GreA	U02878	<i>Rickettsia prowazekii</i>	190	35

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF792	848568	849014	putative				
ORF793	849082	850488	NADH:ubiquinone oxidoreductase subunit A (GP:Z37111 2)	U32702	<i>Haemophilus influenzae</i>	445	37
ORF794	851512	850574	porphobilinogen synthase	U38348	<i>Chlorobium vibrioforme</i>	769	45
ORF795	852064	852447	putative				
ORF796	852398	853690	putative				
ORF797	855118	854243	geranylgeranyl pyrophosphate synthase	D85029	<i>Arabidopsis thaliana</i>	408	41
ORF798	855751	855128	f147; This 147 aa orf is 26 pct identical (1 gaps) to 99 residues of an approx. 728 aa protein E2BE RABIT SW: P47823	AE000143	<i>Escherichia coli</i>	187	36
ORF799	856551	855829	membrane associated regulatory protein	M28368	<i>Salmonella typhimurium</i>	172	36
ORF800	856730	858556	unknown function	Z32530	<i>Chlamydia trachomatis</i>	842	35
ORF801	858717	859601	exodeoxyribonuclease V (recD)	U32811	<i>Haemophilus influenzae</i>	182	51
ORF802	859591	860205	exonuclease V alpha subunit (AA 1-608)	X04582	<i>Escherichia coli</i>	235	45
ORF803	861132	860284	putative				
ORF804	861426	861163	30S ribosomal protein S20	Z67753	<i>Odontella sinensis</i>	153	41
ORF805	861701	862921	putative				
ORF806	863026	864798	major sigma factor	U04442	<i>Chlamydia psittaci</i>	2661	94
ORF807	864831	865256	putative				
ORF808	865226	866581	dihydropterin pyrophosphokinase /dihydropteroate synthase	Y08611	<i>Pisum sativum</i>	455	48
ORF809	866562	867119	dehydrofolate reductase, type I (folA)	U32772	<i>Haemophilus influenzae</i>	213	49
ORF810	867025	867816	M. jannaschii predicted coding region MJ0768	U67522	<i>Methanococcus jannaschii</i>	207	36
ORF811	867820	868497	putative				
ORF812	869743	868661	RecA	U16739	<i>Chlamydia trachomatis</i>	1512	87
ORF813	870633	870094	unknown function	Z32530	<i>Chlamydia trachomatis</i>	308	45
ORF814	871929	870646	unknown function	Z32530	<i>Chlamydia trachomatis</i>	1410	63
ORF815	872538	872086	putative				
ORF816	873908	872517	putative				
ORF817	874281	874670	nifR3-like gene product	Z37984	<i>Azospirillum brasilense</i>	181	32
ORF818	874582	875286	ORF1 gene product	X62399	<i>Escherichia coli</i>	307	42
ORF819	877857	875377	DNA topoisomerase I	L27797	<i>Bacillus subtilis</i>	1488	50

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF820	878446	879255	putative				
ORF821	880635	879268	sigma factor (ntrA) (AA 1-502)	X05888	<i>Azotobacter vinelandii</i>	257	47
ORF822	882524	880593	DNA helicase II	D90906	<i>Synechocystis</i> sp.	1140	50
ORF823	882612	883319	ipa-57d gene product	X73124	<i>Bacillus subtilis</i>	601	51
ORF824	884155	883538	hypothetical protein	D90915	<i>Synechocystis</i> sp.	344	39
ORF825	884340	885611	19/20 residue stretch (32-51) identical to N-terminal putative signal sequence of unknown, partly cloned <i>B. subtilis</i> gene.; putative	L19954	<i>Bacillus subtilis</i>	456	37
ORF826	885722	887302	heat shock protein	L12004	<i>Chlamydia trachomatis</i>	915	39
ORF827	887587	888153	bas1 protein	Z34917	<i>Hordeum vulgare</i>	474	50
ORF828	888627	888220	putative				
ORF829	889330	888716	hypothetical protein	Y14079	<i>Bacillus subtilis</i>	223	55
ORF830	889898	889323	peptidoglycan-associated lipoprotein	X65796	<i>Escherichia coli</i>	222	50
ORF831	891190	889898	TolB	U32470	<i>Haemophilus influenzae</i>	280	35
ORF832	891828	891247	putative				
ORF833	892421	892017	exbD peptide	M28819	<i>Escherichia coli</i>	77	48
ORF834	893116	892421	inner membrane protein (tolQ)	U32722	<i>Haemophilus influenzae</i>	157	54
ORF835	892521	892925	putative				
ORF836	893392	895419	inner membrane copper tolerance protein	Z36905	<i>Escherichia coli</i>	120	35
ORF837	895745	896527	unknown	D26185	<i>Bacillus subtilis</i>	381	41
ORF838	896668	897558	succinate dehydrogenase subunit C	Y08563	<i>Paenibacillus macerans</i>	253	40
ORF839	897565	899442	succinate dehydrogenase subunit A	Y08563	<i>Paenibacillus macerans</i>	1667	57
ORF840	899420	900229	succinate dehydrogenase subunit B	Y08563	<i>Paenibacillus macerans</i>	656	54
ORF841	903230	900237	putative				
ORF842	905081	903234	putative				
ORF843	906931	905045	sigma factor SibG regulation protein RsbU	D90905	<i>Synechocystis</i> sp.	117	35
ORF844	907248	907832	putative				
ORF845	907784	908128	putative				
ORF846	908132	908677	putative				
ORF847	908589	909320	putative				
ORF848	909405	911465	putative				
ORF849	911677	912360	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF850	912303	912821	putative				
ORF851	912937	913983	putative				
ORF852	915128	914067	putative				
ORF853	916658	915303	enolase	L29475	<i>Bacillus subtilis</i>	1036	60
ORF854	915627	915376	enolase	U43738	<i>Mycoplasma pneumoniae</i>	226	65
ORF855	917707	916853	excinuclease ABC subunit B (uvrB)	U32804	<i>Haemophilus influenzae</i>	724	46
ORF856	918837	917722	excinuclease ABC subunit B (uvrB)	U32804	<i>Haemophilus influenzae</i>	1029	54
ORF857	919868	918837	tryptophanyl-tRNA synthetase (trpS)	U32746	<i>Haemophilus influenzae</i>	376	40
ORF858	920434	919880	putative				
ORF859	921187	920438	ORF8	X82078	<i>Chlamydia sp.</i>	164	50
ORF860	921959	921195	hypothetical protein	X62475	<i>Chlamydia psittaci</i>	511	44
ORF861	923773	921995	Threonyl tRNA Synthetase	Z80360	<i>Bacillus subtilis</i>	1476	44
ORF862	922146	922415	putative				
ORF863	923943	923674	putative				
ORF864	924077	925006	putative				
ORF865	925436	925083	putative				
ORF866	926524	925349	putative				
ORF867	927920	926433	putative				
ORF868	928319	927951	putative				
ORF869	928963	928334	putative				
ORF870	929248	930987	DNA mismatch repair protein (mutL)	U32692	<i>Haemophilus influenzae</i>	585	40
ORF871	930995	932059	YqhT	D84432	<i>Bacillus subtilis</i>	445	39
ORF872	932121	933515	putative				
ORF873	932881	932513	putative				
ORF874	933485	935746	pulD (tgg start codon)	M32613	<i>Klebsiella pneumoniae</i>	210	33
ORF875	935724	937082	epsE	M96172	<i>Vibrio cholerae</i>	890	55
ORF876	937229	938410	PilG	U32588	<i>Neisseria gonorrhoeae</i>	280	38
ORF877	938281	938805	putative				
ORF878	938809	939255	putative				
ORF879	939165	939782	putative				
ORF880	939760	940791	putative				
ORF881	940822	941106	putative				
ORF882	940977	941351	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF883	942537	941623	yscT	L25667	<i>Yersinia pseudotuberculosis</i>	169	44
ORF884	942784	942500	yscS	L25667	<i>Yersinia pseudotuberculosis</i>	173	42
ORF885	943149	942799	HrcR	AE000107	<i>Rhizobium sp. NGR234</i>	265	52
ORF886	943799	943029	pathogenicity protein	M64094	<i>Xanthomonas campestris</i>	252	41
ORF887	944055	943732	putative	M74011	<i>Yersinia enterocolitica</i>	112	33
ORF888	944413	943994	putative				
ORF889	945395	944556	putative				
ORF890	945853	945389	putative				
ORF891	946392	945751	HrcJ	U56662	<i>Erwinia amylovora</i>	229	44
ORF892	947410	948081	putative				
ORF893	949871	948915	ORF YOR196c	Z75104	<i>Saccharomyces cerevisiae</i>	702	44
ORF894	951058	949868	dihydrolipoamide dehydrogenase E3 subunit	M57435	<i>Bacillus subtilis</i>	745	39
ORF895	951249	950959	dihydrolipoamide acetyltransferase E3 subunit	M73535	<i>Staphylococcus aureus</i>	166	49
ORF896	951664	952134	putative				
ORF897	952674	952165	SNF	X98455	<i>Bacillus cereus</i>	229	47
ORF898	953491	952589	helicase	U39680	<i>Mycoplasma genitalium</i>	307	42
ORF899	955324	953495	F01G4.1	Z68341	<i>Caenorhabditis elegans</i>	133	57
ORF900	955823	955281	putative				
ORF901	957082	955847	branched-chain amino acid carrier	Z48676	<i>Lactobacillus delbrueckii</i>	297	40
ORF902	957902	957270	endonuclease III	U11289	<i>Bacillus subtilis</i>	317	37
ORF903	959231	957906	homologous to E.coli 50K	X62539	<i>Bacillus subtilis</i>	805	45
ORF904	959376	960284	phosphatidylserine decarboxylase	U72715	<i>Chlamydia trachomatis</i>	776	51
ORF905	960266	961669	putative				
ORF906	961856	964765	secretory component	U06928	<i>Caulobacter crescentus</i>	1812	55
ORF907	966855	965395	28.2% of identity to the Escherichia coli GTP-binding protein Era; putative	L47648	<i>Bacillus subtilis</i>	778	41
ORF908	968204	966975	poly(A) polymerase	L47709	<i>Bacillus subtilis</i>	383	41
ORF909	968791	968237	ClpX-like protein	U18229	<i>Bacillus subtilis</i>	340	39
ORF910	969498	968731	ATP-dependent protease ATPase subunit	D64006	<i>Synechocystis sp.</i>	846	66
ORF911	969858	969511	ClpP	U16135	<i>Synechococcus sp.</i>	257	54



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF912	970118	969762	ATP-dependent clp protease proteolytic component (clpP)	AE000591	<i>Helicobacter pylori</i>	362	63
ORF913	970593	970300	putative				
ORF914	971261	970542	putative				
ORF915	971680	971123	putative				
ORF916	971876	975100	SNF	X98455	<i>Bacillus cereus</i>	778	49
ORF917	975419	976516	MreB protein	M96343	<i>Bacillus subtilis</i>	960	55
ORF918	976584	978320	phospho enol pyruvate carboxykinase	S56812	<i>Chlorobium limicola</i>	1667	64
ORF919	977680	977231	putative				
ORF920	978399	980738	putative				
ORF921	980756	981928	putative				
ORF922	982974	981931	precursor protein (AA -22 to 371)	X52557	<i>Chlamydia trachomatis</i>	97	50
ORF923	984120	983119	NAD+ dependent glycerol-3-phosphate dehydrogenase	L47648	<i>Bacillus subtilis</i>	618	43
ORF924	985502	984120	AgX-1 antigen [human, infertile patient, testis, Peptide, 505 aa]	S73498	<i>Homo sapiens</i>	254	34
ORF925	987180	985882	ORF 4	M72718	<i>Bacillus subtilis</i>	697	38
ORF926	987172	987444	putative				
ORF927	989846	989049	nifU-like protein	AE000542	<i>Helicobacter pylori</i>	302	31
ORF928	991048	989846	putative				
ORF929	991638	990955	phosphoglyceromutase	L09651	<i>Zymomonas mobilis</i>	471	53
ORF930	991794	992498	ORFX13	L09228	<i>Bacillus subtilis</i>	403	39
ORF931	993619	993041	biotin [acetyl-CoA-carboxylase] ligase	L47709	<i>Bacillus subtilis</i>	136	38
ORF932	993530	994792	rod-shape-determining protein	M22857	<i>Escherichia coli</i>	312	44
ORF933	995970	994795	cadmium-transporting ATPase	D64005	<i>Synechocystis sp.</i>	358	47
ORF934	996857	995739	ATPase	L28104	<i>Transposon Tn5422</i>	449	39
ORF935	997603	996782	putative				
ORF936	998969	997572	seryl-trna synthetase	Y09924	<i>Staphylococcus aureus</i>	851	42
ORF937	998896	1000023	orf2, homologue to B.subtilis ribG	X64395	<i>Escherichia coli</i>	596	40
ORF938	1000087	1001340	GTP cyclohydrolase II	D90912	<i>Synechocystis sp.</i>	1078	52
ORF939	1001357	1001818	riboflavin synthase beta subunit	U27202	<i>Actinobacillus pleuropneumoniae</i>	278	36
ORF940	1003288	1001873	putative				
ORF941	1003487	1004146	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF942	1004485	1005639	D-alanine glycine permease (dagA)	AE000603	<i>Helicobacter pylori</i>	394	33
ORF943	1005643	1005972	hypothetical protein MTCY180.08	Z97193	<i>Mycobacterium tuberculosis</i>	274	58
ORF944	1006784	1006116	similar to trithorax protein in final three exons	U13875	<i>Caenorhabditis elegans</i>	155	46
ORF945	1007563	1006769	yycJ	D78193	<i>Bacillus subtilis</i>	406	38
ORF946	1009226	1007568	YtpT	AF008220	<i>Bacillus subtilis</i>	992	47
ORF947	1009989	1009336	putative				
ORF948	1015852	1016337	putative				
ORF949	1016561	1016181	putative				
ORF950	1016297	1017532	putative				
ORF951	1016802	1016452	putative				
ORF952	1018993	1017701	phenolhydroxylase component	U32702	<i>Haemophilus influenzae</i>	909	47
ORF953	1019454	1019137	ORF	M63939	<i>Escherichia coli</i>	96	45
ORF954	1020764	1019562	pCTHm1 gene product	M94254	<i>Chlamydia trachomatis</i>	1185	65
ORF955	1021405	1021037	histone H1-like protein	M80324	<i>Chlamydia psittaci</i>	319	62
ORF956	1021821	1024286	phosphoprotein	L25078	<i>Chlamydia trachomatis</i>	739	41
ORF957	1024697	1024248	putative				
ORF958	1025569	1024508	protoporphyrinogen oxidase	U25114	<i>Mus musculus</i>	86	38
ORF959	1026969	1025590	oxygen independent coprophorphyrinogen III oxidase	D90912	<i>Synechocystis sp.</i>	880	42
ORF960	1027789	1026947	uroporphyrinogen decarboxylase	M97208	<i>Bacillus subtilis</i>	372	38
ORF961	1031199	1027945	transcription-repair coupling factor (trcF) (mfd)	U32805	<i>Haemophilus influenzae</i>	1584	42
ORF962	1031717	1031172	alanyl-tRNA synthetase	X95571	<i>Thiobacillus ferrooxidans</i>	76	31
ORF963	1033057	1031612	alanyl-tRNA synthetase	AE000353	<i>Escherichia coli</i>	889	40
ORF964	1033425	1033039	alanyl-tRNA synthetase (alaS)	AE000629	<i>Helicobacter pylori</i>	327	51
ORF965	1033784	1033200	alanyl-tRNA synthetase	X59956	<i>Rhizobium leguminosarum</i>	416	47
ORF966	1033963	1036038	transketolase	Z73234	<i>Bacillus subtilis</i>	1398	44
ORF967	1036945	1036010	AMP nucleosidase	AE000290	<i>Escherichia coli</i>	265	42
ORF968	1037110	1037679	elongation factor P	U14003	<i>Escherichia coli</i>	458	51
ORF969	1037696	1037944	putative				
ORF970	1038916	1037975	putative				
ORF971	1040582	1039026	HSP60 chaperonin	X62914	<i>Clostridium perfringens</i>	284	31

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF972	1040997	1042337	PROBABLE UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2, 6-DIAMINOLIGASE (EC 6.3.2.15)	AB001488	<i>Bacillus subtilis</i>	446	39
ORF973	1042357	1043403	ORF-Y (AA 1-360)	X51584	<i>Escherichia coli</i>	582	45
ORF974	1043367	1044623	UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD)	U32793	<i>Haemophilus influenzae</i>	348	42
ORF975	1044607	1045362	hypothetical protein	Y14079	<i>Bacillus subtilis</i>	115	38
ORF976	1045384	1046538	spoVE gene product (AA 1-366)	X51419	<i>Bacillus subtilis</i>	479	35
ORF977	1046447	1047517	mur	Y13922	<i>Enterococcus hirae</i>	256	45
ORF978	1047521	1049956	UDP-N-acetylmuramate-alanine ligase (murC)	U32794	<i>Haemophilus influenzae</i>	756	38
ORF979	1050611	1050036	unknown	Z74024	<i>Mycobacterium tuberculosis</i>	78	44
ORF980	1050925	1050566	cycY gene product	U14003	<i>Escherichia coli</i>	179	34
ORF981	1051728	1051090	putative				
ORF982	1051743	1052063	hypothetical protein	D90908	<i>Synechocystis sp.</i>	135	33
ORF983	1052101	1053126	trna delta(2)-isopentenylpyrophosphate transferase	Z98209	<i>Mycobacterium tuberculosis</i>	441	37
ORF984	1054201	1053107	conserved hypothetical protein	AE000579	<i>Helicobacter pylori</i>	826	44
ORF985	1054242	1055555	putative				
ORF986	1055483	1055908	putative				
ORF987	1056609	1056965	YqeL	D84432	<i>Bacillus subtilis</i>	202	38
ORF988	1056961	1058232	beta-ketoacyl-ACP synthase	L13242	<i>Ricinus communis</i>	1266	55
ORF989	1058238	1058687	diadenosine tetraphosphatase	U30313	<i>Homo sapiens</i>	122	42
ORF990	1059371	1058727	inorganic pyrophosphatase (ppa)	AE000576	<i>Helicobacter pylori</i>	209	39
ORF991	1059526	1060578	leucine dehydrogenase LeuDH	U51099	<i>Bacillus cereus</i>	680	45
ORF992	1061553	1060579	3'(2'),5'-bisphosphate nucleotidase	U40433	<i>Arabidopsis thaliana</i>	335	43
ORF993	1061674	1062411	putative				
ORF994	1062377	1064077	2-acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase	U29581	<i>Escherichia coli</i>	383	44
ORF995	1064116	1065243	7-keto-8-aminopelargonic acid synthetase (bioF)	M29291	<i>Bacillus sphaericus</i>	200	35
ORF996	1067451	1065178	priA	Y10304	<i>Bacillus subtilis</i>	1009	43

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF997	1068065	1067376	putative				
ORF998	1068209	1068706	putative				
ORF999	1069958	1068819	unknown	U41759	<i>Chlamydia psittaci</i>	777	41
ORF1000	1071163	1070033	unknown	U41759	<i>Chlamydia psittaci</i>	381	36
ORF1001	1072438	1071332	unknown	U41759	<i>Chlamydia psittaci</i>	254	37
ORF1002	1072997	1073476	putative				
ORF1003	1074239	1075864	lysyl-tRNA synthetase	D90906	<i>Synechocystis</i> sp.	1007	48
ORF1004	1076790	1075867	cysteinyI-tRNA synthetase	L14580	<i>Bacillus subtilis</i>	395	52
ORF1005	1077268	1076573	cys-tRNA synthetase (cysS)	U32693	<i>Haemophilus influenzae</i>	431	56
ORF1006	1077999	1078724	putative				
ORF1007	1079088	1078672	ribonuclease P protein component (gtg start codon)	M11056	<i>Escherichia coli</i>	78	46
ORF1008	1079642	1079944	30S ribosomal subunit protein S14	U18997	<i>Escherichia coli</i>	260	50
ORF1009	1080501	1079995	F18C12.2	Z75536	<i>Caenorhabditis elegans</i>	118	38
ORF1010	1080775	1081341	putative				
ORF1011	1083158	1081350	deoxyribodipyrimidine photolyase	J03294	<i>Bacillus subtilis</i>	687	44
ORF1012	1084677	1083235	DNA mismatch repair protein	U71154	<i>Aquifex pyrophilus</i>	735	48
ORF1013	1085648	1084632	DNA mismatch repair protein	D90909	<i>Synechocystis</i> sp.	565	39
ORF1014	1086117	1086737	DNA primase (dnaG)	U32735	<i>Haemophilus influenzae</i>	303	40
ORF1015	1086692	1087897	DnaG	Z83860	<i>Mycobacterium tuberculosis</i>	222	37
ORF1016	1088646	1089005	putative				
ORF1017	1089146	1089805	putative				
ORF1018	1092931	1089890	glycyl-tRNA synthetase	U20547	<i>Chlamydia trachomatis</i>	2569	48
ORF1019	1093179	1092889	putative				
ORF1020	1093584	1094204	phosphatidylglycerophosphate synthase	U87792	<i>Bacillus subtilis</i>	163	55
ORF1021	1095619	1094192	glycogen (starch) synthase	D90899	<i>Synechocystis</i> sp.	574	40
ORF1022	1096074	1096628	partial ctc gene product (AA 1-186)	X16518	<i>Bacillus subtilis</i>	86	37
ORF1023	1096633	1097082	peptidyl-tRNA hydrolase	U31570	<i>Chlamydia trachomatis</i>	378	53
ORF1024	1097266	1097601	ribosomal protein S6 (rps6)	AE000630	<i>Helicobacter pylori</i>	179	39
ORF1025	1097622	1097867	ribosomal protein S18 homolog; putative	M62820	<i>Chlamydia trachomatis</i>	324	86
ORF1026	1097886	1098392	putative heat shock protein ORF; putative	M62820	<i>Chlamydia trachomatis</i>	190	79
ORF1027	1099521	1099279	putative				
ORF1028	1099689	1101053	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1029	1102192	1101107	putative				
ORF1030	1104950	1102116	glycerol-3-phosphate acyltransferase	M80571	<i>Cucumis sativus</i>	574	43
ORF1031	1106508	1104946	ORF_f495; orfF of ECMRED, uses 2nd start	U18997	<i>Escherichia coli</i>	855	38
ORF1032	1106722	1107249	putative				
ORF1033	1107463	1108101	PlsX	U59433	<i>Bacillus subtilis</i>	282	45
ORF1034	1108041	1108421	fatty acid/phospholipid synthesis protein (plsX)	AE000540	<i>Helicobacter pylori</i>	205	35
ORF1035	1108520	1113370	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	352	44
ORF1036	1114958	1113447	putative				
ORF1037	1116915	1115071	lipid A disaccharide synthetase (lpxB)	U32786	<i>Haemophilus influenzae</i>	477	42
ORF1038	1118183	1116894	poly(A) polymerase	AE000123	<i>Escherichia coli</i>	555	46
ORF1039	1118846	1120030	putative	L12968	<i>Escherichia coli</i>	880	50
ORF1040	1120040	1120522	glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS)	AE000651	<i>Helicobacter pylori</i>	396	52
ORF1041	1120510	1121430	glutamine amidotransferase; glucosamine--fructose-6-phosphate aminotransferase	AE000450	<i>Escherichia coli</i>	494	44
ORF1042	1121321	1121866	L-glutamine:D-fructose-6-P amidotransferase precursor	U17352	<i>Thermus aquaticus thermophilus</i>	374	50
ORF1043	1122123	1122899	tyrosine-specific transport protein	AE000284	<i>Escherichia coli</i>	281	41
ORF1044	1124842	1125564	putative				
ORF1045	1126526	1125579	cell division protein (flsY)	U32760	<i>Haemophilus influenzae</i>	497	41
ORF1046	1126519	1127676	succinyl-CoA synthetase beta-subunit	J01619	<i>Escherichia coli</i>	784	43
ORF1047	1127672	1128571	succinyl coenzyme A synthetase alpha subunit	U23408	<i>Dictyostelium discoideum</i>	978	63
ORF1048	1130230	1131336	putative				
ORF1049	1131480	1132553	putative				
ORF1050	1132830	1133843	putative				
ORF1051	1134121	1134855	serine protease HtrA	D90905	<i>Synechocystis sp.</i>	307	51
ORF1052	1134642	1135592	GsrA protein	D78376	<i>Yersinia enterocolitica</i>	497	41
ORF1053	1135964	1135653	putative				
ORF1054	1137132	1135954	R11H6.1	Z93386	<i>Caenorhabditis elegans</i>	445	37
ORF1055	1137169	1140102	Ydr430cp; CAI: 0.15	U33007	<i>Saccharomyces cerevisiae</i>	559	40

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1056	1141365	1140112	hypothetical 54.7 kD protein in udp 3' region precursor (o475)	AE000459	<i>Escherichia coli</i>	222	34
ORF1057	1142150	1141356	phosphatidylserine synthase (pssA)	AE000614	<i>Helicobacter pylori</i>	307	41
ORF1058	1142520	1145660	ribonucleotide reductase subunit M1	K02927	<i>Mus musculus</i>	1433	45
ORF1059	1145627	1146721	ribonucleoside diphosphate reductase, beta subunit (nrdB)	AE000553	<i>Helicobacter pylori</i>	443	32
ORF1060	1146862	1147545	unknown	Z95398	<i>Mycobacterium leprae</i>	191	35
ORF1061	1147666	1148190	YtqB	AF008220	<i>Bacillus subtilis</i>	262	44
ORF1062	1148514	1148224	ORF2	U01958	<i>Bacillus licheniformis</i>	135	54
ORF1063	1149136	1148348	ORF2	M31827	<i>Bacillus subtilis</i>	268	40
ORF1064	1149702	1149166	putative				
ORF1065	1150031	1150591	unknown	Z85982	<i>Mycobacterium tuberculosis</i>	445	49
ORF1066	1150785	1151147	ribosomal protein L20 (AA 1-119)	X16188	<i>Bacillus stearothermophilus</i>	273	44
ORF1067	1151165	1152181	phenylalanyl-tRNA synthetase beta subunit	Z75208	<i>Bacillus subtilis</i>	777	40
ORF1068	1152522	1154591	putative				
ORF1069	1155666	1154566	putative				
ORF1070	1156743	1155670	putative				
ORF1071	1156859	1157815	hypothetical	U32723	<i>Haemophilus influenzae</i>	252	42
ORF1072	1157982	1160735	ATP-binding protein	U01376	<i>Escherichia coli</i>	1314	56
ORF1073	1162620	1160917	polynucleotide phosphorylase	AF010578	<i>Pisum sativum</i>	1416	52
ORF1074	1162970	1162590	polynucleotide phosphorylase	U52048	<i>Spinacia oleracea</i>	312	53
ORF1075	1163532	1164020	orf150 gene product	X95938	<i>Porphyromonas gingivalis</i>	335	43
ORF1076	1163995	1164294	putative				
ORF1077	1165569	1165030	putative				
ORF1078	1166108	1165566	putative				
ORF1079	1166644	1166141	putative				
ORF1080	1167055	1168374	putative				
ORF1081	1169218	1168337	methionine aminopeptidase	D64003	<i>Synechocystis sp.</i>	488	54
ORF1082	1169823	1169218	ORF o197	U18997	<i>Escherichia coli</i>	281	30
ORF1083	1171324	1170572	putative				
ORF1084	1172085	1171177	hypothetical	U32720	<i>Haemophilus influenzae</i>	162	44
ORF1085	1172394	1173773	fumarase	D64000	<i>Synechocystis sp.</i>	1292	57
ORF1086	1175209	1173881	prs-associated putative membrane protein	U02424	<i>Escherichia coli</i>	570	39



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1087	1175555	1175127	hypothetical protein in pth-prs intergenic region	AE000219	<i>Escherichia coli</i>	278	46
ORF1088	1175778	1177043	hypothetical protein	Z96072	<i>Mycobacterium tuberculosis</i>	109	43
ORF1089	1177177	1179048	putative				
ORF1090	1179156	1180085	penicillin tolerance protein (lytB)	U32781	<i>Haemophilus influenzae</i>	731	54
ORF1091	1180045	1180779	putative				
ORF1092	1181942	1180788	putative				
ORF1093	1182296	1181961	putative				
ORF1094	1183844	1182300	putative				
ORF1095	1184420	1183848	putative				
ORF1096	1185382	1184366	putative				
ORF1097	1185858	1185226	putative				
ORF1098	1186164	1186481	putative				
ORF1099	1187386	1186484	site-specific recombinase	U92524	<i>Salmonella typhimurium</i>	401	48
ORF1100	1187370	1189028	phosphoglucosomerase-like protein	L40822	<i>Chlamydia trachomatis</i>	1154	63
ORF1101	1189321	1190889	putative				
ORF1102	1191142	1192146	NADP-malate dehydrogenase	L40958	<i>Flaveria bidentis</i>	775	46
ORF1103	1191974	1191729	putative				
ORF1104	1193815	1192991	putative				
ORF1105	1195702	1194248	o460; This 460 aa orf is 46 pct identical (26 gaps) to 458 residues of an approx. 488 aa protein ARCD PSEAE SW: P18275	AE000256	<i>Escherichia coli</i>	1022	44
ORF1106	1196303	1195716	putative				
ORF1107	1196831	1196337	putative				
ORF1108	1197807	1196746	putative				
ORF1109	1198740	1197883	putative				
ORF1110	1200232	1198721	shikimate 5-dehydrogenase	U67551	<i>Methanococcus jannaschii</i>	245	37
ORF1111	1201286	1200135	3-dehydroquinate synthase (aroB)	U32705	<i>Haemophilus influenzae</i>	478	45
ORF1112	1202386	1201259	2,3-dihydroxybenzoic acid	L29562	<i>Vibrio anguillarum</i>	780	50
ORF1113	1202901	1202350	putative				
ORF1114	1204162	1202816	5-enolpyruvylshikimate 3-phosphate synthase	U67500	<i>Methanococcus jannaschii</i>	520	40
ORF1115	1203177	1203464	putative				



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1116	1205028	1204180	putative				
ORF1117	1206392	1204878	bioA gene product	A02587	unidentified	834	48
ORF1118	1206742	1206086	dethiobiotin synthase (bioD)	U32830	<i>Haemophilus influenzae</i>	243	37
ORF1119	1207872	1206724	L-alanine - pimelyl CoA ligase	U51868	<i>Bacillus subtilis</i>	601	41
ORF1120	1208852	1207851	biotin synthase	U24147	<i>Arabidopsis thaliana</i>	892	52
ORF1121	1210518	1209742	tryptophan hydroxylase	U26428	<i>Gallus gallus</i>	237	34
ORF1122	1210703	1211494	dihydrodipicolinate reductase	U47017	<i>Pseudomonas syringae pv. tabaci</i>	345	37
ORF1123	1211870	1212754	aspartate-semialdehyde dehydrogenase	U67476	<i>Methanococcus jannaschii</i>	444	43
ORF1124	1212742	1214064	aspartokinase III	U00006	<i>Escherichia coli</i>	473	47
ORF1125	1214046	1214858	dihydrodipicolinate synthase	D64006	<i>Synechocystis sp.</i>	238	40
ORF1126	1215551	1216318	putative				
ORF1127	1216493	1216849	putative				
ORF1128	1217183	1219612	putative				
ORF1129	1220068	1219673	putative				
ORF1130	1219710	1220669	putative				
ORF1131	1220630	1221376	putative				
ORF1132	1221645	1223681	unknown	D26185	<i>Bacillus subtilis</i>	621	43
ORF1133	1223894	1224988	putative				
ORF1134	1225000	1225830	high level kasamycin resistance	D26185	<i>Bacillus subtilis</i>	422	41
ORF1135	1227810	1225879	hypothetical protein	D90903	<i>Synechocystis sp.</i>	1129	43
ORF1136	1226528	1226908	putative				
ORF1137	1229972	1228311	exonuclease VII, large subunit (xseA)	U32723	<i>Haemophilus influenzae</i>	666	46
ORF1138	47569	47018	Integrase/recombinase	AE001308	<i>Chlamydia trachomatis</i>	716	72
ORF1139	49980	49117	putative				
ORF1140	53356	52898	putative				
ORF1141	54477	54884	O-Sialoglycoprotein Endopeptidase	AE001307	<i>Chlamydia trachomatis</i>	311	51
ORF1142	63753	63998	PTS PEP Phosphotransferase	AE001306	<i>Chlamydia trachomatis</i>	198	61
ORF1143	77164	77487	putative				
ORF1144	79724	79302	Sms Protein	AE001302	<i>Chlamydia trachomatis</i>	458	57
ORF1145	88721	88951	putative				
ORF1146	94067	94429	putative				
ORF1147	122832	123341	hypothetical protein	AE001303	<i>Chlamydia trachomatis</i>	398	61
ORF1148	147536	147234	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1149	158990	159346	S16 Ribosomal Protein	AE001277	<i>Chlamydia trachomatis</i>	467	78
ORF1150	168470	168979	putative				
ORF1151	169183	169452	putative				
ORF1152	171785	171504	Cationic Amino Acid Transporter	AE001278	<i>Chlamydia trachomatis</i>	262	68
ORF1153	172518	171775	Cationic Amino Acid Transporter	AE001278	<i>Chlamydia trachomatis</i>	533	48
ORF1154	193599	194045	putative				
ORF1155	195704	196075	S/T Protein Kinase	AE001288	<i>Chlamydia trachomatis</i>	536	82
ORF1156	210687	210145	KDO-transferase	X80061	<i>Chlamydia pneumoniae</i>	856	96
ORF1157	211100	210708	putative				
ORF1158	215420	215088	putative				
ORF1159	217914	218246	putative				
ORF1160	218925	218701	putative				
ORF1161	223785	223525	IMP dehydrogenase	U13372	<i>Borrelia burgdorferi</i>	270	63
ORF1162	224271	223999	putative				
ORF1163	228691	228407	putative				
ORF1164	235050	235334	(Methylase)	AE001287	<i>Chlamydia trachomatis</i>	331	66
ORF1165	252308	253021	Oligopeptide Permease	AE001293	<i>Chlamydia trachomatis</i>	838	72
ORF1166	258280	258912	Dicarboxylate Translocator	AE001294	<i>Chlamydia trachomatis</i>	909	80
ORF1167	261325	261567	putative				
ORF1168	268195	268878	hypothetical protein	AE001287	<i>Chlamydia trachomatis</i>	556	52
ORF1169	269447	268881	putative				
ORF1170	271263	271538	putative				
ORF1171	271957	272346	putative				
ORF1172	274176	274550	putative				
ORF1173	275736	275314	Disulfide bond Oxidoreductase	AE001291	<i>Chlamydia trachomatis</i>	519	73
ORF1174	276490	276927	hypothetical protein	AE001291	<i>Chlamydia trachomatis</i>	249	53
ORF1175	277577	277861	hypothetical protein	AE001291	<i>Chlamydia trachomatis</i>	256	52
ORF1176	288163	287909	putative				
ORF1177	290130	289789	putative				
ORF1178	290989	291225	putative				
ORF1179	291372	291860	adenylate cyclase	AE001286	<i>Chlamydia trachomatis</i>	388	48
ORF1180	311239	311622	putative				
ORF1181	328665	328384	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1182	337348	338289	sodium-dependent transporter	AF017105	<i>Chlamydia psittaci</i>	1112	72
ORF1183	364764	364369	Prolipoprotein Diacylglycerol Transferase	AE001298	<i>Chlamydia trachomatis</i>	300	54
ORF1184	389623	390135	hypothetical protein	AE001282	<i>Chlamydia trachomatis</i>	75	33
ORF1185	393729	394343	ABC superfamily ATPase	AE001282	<i>Chlamydia trachomatis</i>	473	52
ORF1186	407379	407621	putative				
ORF1187	410944	410708	putative				
ORF1188	427632	427988	putative				
ORF1189	428172	428486	putative				
ORF1190	436761	437246	hypothetical protein	AE001279	<i>Chlamydia trachomatis</i>	661	81
ORF1191	460911	461159	putative				
ORF1192	477597	477313	hypothetical protein	AE001300	<i>Chlamydia trachomatis</i>	309	62
ORF1193	487303	487001	putative				
ORF1194	487764	487534	Glycine Cleavage System H Protein	AE001300	<i>Chlamydia trachomatis</i>	221	67
ORF1195	498502	499017	hypothetical protein	AE001275	<i>Chlamydia trachomatis</i>	206	32
ORF1196	499795	500466	putative				
ORF1197	571928	572344	putative				
ORF1198	572367	572131	putative				
ORF1199	588184	587915	hypothetical protein	AE001312	<i>Chlamydia trachomatis</i>	256	62
ORF1200	600587	600907	(Metalloenzyme)	AE001316	<i>Chlamydia trachomatis</i>	314	61
ORF1201	609731	608895	putative				
ORF1202	614039	614755	hypothetical protein	AE001317	<i>Chlamydia trachomatis</i>	475	46
ORF1203	614823	615152	putative				
ORF1204	638244	638831	ABC Transporter ATPase	AE001315	<i>Chlamydia trachomatis</i>	614	61
ORF1205	638819	639094	(Metal Transport Protein)	AE001315	<i>Chlamydia trachomatis</i>	265	63
ORF1206	639073	639636	(Metal Transport Protein)	AE001315	<i>Chlamydia trachomatis</i>	687	69
ORF1207	647901	648236	hypothetical protein	AE001317	<i>Chlamydia trachomatis</i>	139	38
ORF1208	678510	679469	phosphohydrolase	AE001320	<i>Chlamydia trachomatis</i>	995	63
ORF1209	688178	688732	hypothetical protein	AE001320	<i>Chlamydia trachomatis</i>	366	43
ORF1210	696045	696563	methyltransferase	AE001321	<i>Chlamydia trachomatis</i>	369	49
ORF1211	708998	708588	Glucose-1-P Adenyltransferase	AE001322	<i>Chlamydia trachomatis</i>	507	83
ORF1212	709808	710089	putative				
ORF1213	718240	717737	Glycerol-3-P Phosphatidyltransferase	AE001323	<i>Chlamydia trachomatis</i>	573	66
ORF1214	737828	737565	S19 Ribosomal Protein	AE001323	<i>Chlamydia trachomatis</i>	439	94

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1215	779502	780257	hypothetical protein	AE001322	<i>Chlamydia trachomatis</i>	476	48
ORF1216	806310	805864	hypothetical protein	AE001337	<i>Chlamydia trachomatis</i>	512	67
ORF1217	820931	820707	putative				
ORF1218	837696	839096	Exodeoxyribonuclease V, Gamma	AE001334	<i>Chlamydia trachomatis</i>	967	49
ORF1219	883307	883549	putative				
ORF1220	892010	891726	putative				
ORF1221	893277	893564	putative				
ORF1222	936998	937225	Gen. Secretion Protein E	AE001327	<i>Chlamydia trachomatis</i>	256	67
ORF1223	946865	947419	putative				
ORF1224	975187	975411	SWF/SNF family helicase	AE001341	<i>Chlamydia trachomatis</i>	363	96
ORF1225	985882	985517	hypothetical protein	AE001342	<i>Chlamydia trachomatis</i>	166	33
ORF1226	987713	987180	hypothetical protein	AE001342	<i>Chlamydia trachomatis</i>	447	59
ORF1227	988215	987733	Flagellar M-Ring Protein	AE001342	<i>Chlamydia trachomatis</i>	304	44
ORF1228	988754	988530	Flagellar M-Ring Protein	AE001342	<i>Chlamydia trachomatis</i>	92	36
ORF1229	992542	992841	hypothetical protein	AE001343	<i>Chlamydia trachomatis</i>	112	39
ORF1230	992759	993067	hypothetical protein	AE001343	<i>Chlamydia trachomatis</i>	100	32
ORF1231	1004247	1004528	D-Ala/Gly Permease	AE001344	<i>Chlamydia trachomatis</i>	283	64
ORF1232	1015013	1014294	235aa long hypothetical protein	AB009472	<i>Pyrococcus horikoshii</i>	104	54
ORF1233	1056147	1056545	putative				
ORF1234	1077682	1078035	predicted disulfide bond isomerase	AE001351	<i>Chlamydia trachomatis</i>	233	46
ORF1235	1088121	1088381	putative				
ORF1236	1098430	1098852	Predicted Kinase	AE001352	<i>Chlamydia trachomatis</i>	384	59
ORF1237	1098798	1099319	Predicted Kinase	AE001352	<i>Chlamydia trachomatis</i>	322	45
ORF1238	1123198	1123515	Transport Permease	AE001354	<i>Chlamydia trachomatis</i>	313	72
ORF1239	1123606	1124256	Tyrosine Transport	AE001354	<i>Chlamydia trachomatis</i>	577	58
ORF1240	1124453	1124797	Tyrosine Transport	AE001354	<i>Chlamydia trachomatis</i>	323	50
ORF1241	1129253	1129567	putative				
ORF1242	1164947	1164474	hypothetical protein	AE001357	<i>Chlamydia trachomatis</i>	412	56
ORF1243	1170457	1170053	hypothetical protein	AE001358	<i>Chlamydia trachomatis</i>	283	59
ORF1244	1172342	1171863	ABC transporter permease	AE001358	<i>Chlamydia trachomatis</i>	457	55
ORF1245	1192155	1192835	putative				
ORF1246	1192759	1192992	putative				
ORF1247	1193861	1194142	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1248	1194036	1193779	(D-Amino Acid Dehydrogenase)	AE001311	<i>Chlamydia trachomatis</i>	269	79
ORF1249	1209748	1209053	conserved hypothetical protein	AE000958	<i>Archaeoglobus fulgidus</i>	121	38
ORF1250	1215111	1215419	putative				
ORF1251	1216302	1216538	putative				
ORF1252	1228072	1227818	hypothetical protein	AE001306	<i>Chlamydia trachomatis</i>	134	39
ORF1253	1228304	1228080	xseB	AL021897	<i>Mycobacterium tuberculosis</i>	89	33
ORF1254	26599	26222	putative				
ORF1255	27609	27367	putative				
ORF1256	67206	66967	putative				
ORF1257	70612	70352	putative				
ORF1258	132703	132945	putative				
ORF1259	178073	178393	putative				
ORF1260	208576	208349	putative				
ORF1261	209156	208929	putative				
ORF1262	209263	209024	putative				
ORF1263	210304	210639	putative				
ORF1264	299009	299452	putative				
ORF1265	352106	351717	putative				
ORF1266	420182	419949	Flagellar Secretion Protein	AE001280	<i>Chlamydia trachomatis</i>	115	43
ORF1267	553602	553381	putative				
ORF1268	556538	556807	putative				
ORF1269	594348	593797	putative				
ORF1270	595169	594876	putative				
ORF1271	662148	662381	putative				
ORF1272	706528	706893	putative				
ORF1273	803315	803650	putative				
ORF1274	849551	849306	putative				
ORF1275	913676	913275	putative				
ORF1276	927087	926836	putative				
ORF1277	930587	930360	putative				
ORF1278	986531	986764	ORF 12	M72718	<i>Bacillus subtilis</i>	106	48
ORF1279	996229	996486	putative				
ORF1280	1000373	1000002	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1281	1010291	1010037	putative				
ORF1282	1011128	1010793	106aa long hypothetical protein	AB009472	<i>Pyrococcus horikoshii</i>	159	50
ORF1283	1012924	1012694	putative				
ORF1284	1028659	1028913	putative				
ORF1285	1086481	1086762	putative				
ORF1286	1118658	1118879	Phosphoglucosyltransferase	AE001354	<i>Chlamydia trachomatis</i>	291	84
ORF1287	1170098	1169835	hypothetical protein	AE001358	<i>Chlamydia trachomatis</i>	187	53
ORF1288	1180828	1181184	putative				
ORF1289	1182658	1183035	putative				
ORF1290	1195076	1194795	putative				
ORF1291	1195890	1196183	putative				